

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 102278

To: Sheridan Swope

Location: CM1-10D01

Art Unit: 1652

Wednesday, August 27, 2003

Case Serial Number: 09/696872

From: Beverly Shears

Location: Biotech-Chem Library

CM1-1E05

Phone: 308-4994

beverly.shears@uspto.gov

Search Notes		
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From: Sent:

Swope, Sheridan

Monday, August 25, 2003 6:21 PM STIC-Biotech/ChemLib

To: Subject:

FW: 09696872

-----Original Message----

From:

Chan, Christina

Sent: To: Monday, August 25, 2003 6:20 PM Swope, Sheridan; STIC-Biotech/ChemLib

Subject:

RE: 09696872

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644 308-3973 CM-1, 9B19

-----Original Message-----

From:

Swope, Sheridan

Sent:

Monday, August 25, 2003 5:18 PM

To:

Chan, Christina

Subject:

09696872

May I have this rushed?

For 09696872, pls search:

SID 23 against the AA and NT data bases.

SID 24 against the AA and NT data bases.

SID 37 against the AA and NT data bases.

Sheridan Swope, Ph.D.
Patent Examiner, AU 1652
Recombinant Enzymes
sheridan.swope@uspto.gov
703-305-1696 (voice)
703-308-3014 (FAX)
Mailbox: CM1 Rm10D01
Office: CM1 Rm12D12

Searcher:
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Online time:

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NA Sequences:
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Other

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SEARCH REQUEST FORM

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-DB-GenZmbl -QFMT=fastap -SUPFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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SUMMARIES

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Rothman, J.E., Mayhew, M. and Hoe, M.H. KDEL receptor inhibitors
Patent: US 616,088-A 24,12-DEC-2000;
                                              1 (bases 1 to 372)
Rothman, J.E., Mayhew, M. and Hoe, M.H.
KDEL receptor inhibitors
Patent: US 6160088-A 30 12-DEC-2000;
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 GluThrAsnAlaAlaLeuGlnAspValArgAspTrpLeuArgGlnGlnValArgGluIle
                                            SerSerLeuGlyGlyAspCysCysSerAspLeuGlyProGlnMetLeuArgGluLeuGln
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RESULT 5
AR121632
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Sequence 16
AR121624
AR121624.1
 AR121632
Sequence
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Rothman, J.E., Mayhew, M. and Hoe, M.H.
KDEL receptor inhibitors
Patent: US 6160088-A 16 12-DEC-2000;
Location/Qualifiers
1. 387
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Unclassified.
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                                                             ProGluGlyThrGlySerSerGluLysAspGluLeu
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                                                                                                                                               ValMetGluCysAspAlaCysGly------
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AR121623
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AUTHORS
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Sequence
AR121623
AR121623.
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Rothman, J.E., Mayhew, M. and Hoe, M.H.
KDEL receptor inhibitors
Patent: US 6160088-A 35 12-DEC-2000,
Location/Qualifiers
                                                                                                                                1 (bases 1 to 387)
Rothman, J.E., Mayhew, M. and Hoe, M.H.
KDEL receptor inhibitors
Patent: US 6160088-A 14 12-DEC-2000;
                                                                                                                                                                         Unclassified
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AR121632.1
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|CAGGAGACTAATGCGGCGCTGCAAGACGTGAGAGAGCTCTTGCGACAGCAGGTCAAGGAG
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122 c 134 g
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7.05e-30
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from patent US 6160088.
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Sequence 22
AR121627
AR121627.1
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                                                                                                                                                                                                                                                                             1 (bases 1 to 369)
Rothman, J.E., Mayhew, M. and Hoe, M.H.
KDEL receptor inhibitors
Patent: US 6160088-A 22 12-DEC-2000;
Location/Qualifiers
1. 369
                                                                                                                                                                                                                                                                                                                                            Unknown
                                                                                                                                                                                                                                                                                                                                  Unclassified
                                                                                                                                                                                                                                                                                                                                                    Unknown.
                                                      GlnAspValArgAspTrpLeuArgGlnGlnValArgGluIleThrPheLeuLysAsnThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CysCysSerAspLeuGlyProGlnMetLeuArgGluLeuGlnGluThrAsnAlaAlaLeu 47
                                             GGAGAGCTCCGÁGATGTCATGAGACAGCAGGTGAAAGAGACCATGTTCTTGAGAAACACC
                                                                                                                              LeuLeuAlaLeuAlaAlaValCysSerAlaAlaLysLysGlySerSerLeuGlyGlyAsp
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                     ValMetGluCysAspAlaCysGlyProGlnProGlnProLysProGlnProGlnProGln
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                                                                                 TGTTGTGGTGACGTCAGCAGACAGTTGATTGGCCAGATAACCCAAATGAATCAGATGCTG
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94 c 121 g
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63.61%
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US 6160088
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Matches:
Conservative:
Mismatches:
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Gaps:
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                 RESULT 9
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Sequence 18
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Sequence 20
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1 (bases 1 to 369)

Rothman, J.E., Mayhew, M. and Hoe, M.H.

KDEL receptor inhibitors

Patent: US 6160088-A 20 12-DEC-2000;

Location/Qualifiers
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ATCATGGAGTGTCAGGTGTGCGGTCCGCAGCCGCAGCCGAAACCGCAGCCGCAGCCGCAG
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                                                                                                                                                                   ProGlnProLysProGlnProLysProGluProGluGlyThrGlySerSerGluLysAsp
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Rothman, J.E., Mayhew, M. and Hoe, M.H.
KDEL receptor inhibitors
Patent: US 6160088-A 26 12-DEC-2000;
Location/Qualifiers
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Sequence 26 from patent
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KDEL receptor inhibitors
Patent: US 6160088-A 18 12-DEC-2000;
Location/Qualifiers
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Submitted (27-JUN-2002) Hiroshi Mori, Osaka City University Medical School, Neuroscience; 1-4-3 Asahimachi, Abenoku, Osaka 545-8585, Japan (E-mail:mori@med.osaka-cu.ac.jp, Tel:81-6-6645-3920,
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AB086984
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Human comp cDNA with 5
Unpublished
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Hashimoto, Y. and Mori, H.
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Mammalia; Eutheria; Primates;
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DPGLAVGYTAFNGVDFEGTFHVNTVTDDDYAGF I FGYQDSSS FYVVMWKQMEQTYWQA
NPFRAVAEPGI QLKAVKSSTGPGEQLRNALMHTGDTESQVRLLMKD PRNVGWKDKKSY
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/codon_start=1
/product="cartilage oligomeric matrix protein"
/protein id="BAC53888.1"
/protein id="BAC538066"
/db_xref="GI:27530066"
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/replace="c"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequence 1426 from Patent WO0194629
AX330917
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Sequence 1207 from Patent WO0194629
AX330698
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
             Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z.
Cancer gene determination and therapeutic screening using signature
                                                                                                                                                               AX330917.1 GI:18103896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent: WO 0194629-A 1207 13-DEC-2001; Avalon Pharmaceuticals (US)
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Cancer gene determination and therapeutic screening using s
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/db_xref="taxon:9606"
758 c 809 g 36
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Patent: WO 0194629-A 1426 13-DEC-2001;
Avalon Pharmaceuticals (US)
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Newton,G., Weremowicz,S., Morton,C.C., Copeland,N.G., Gilbert,D.J Jenkins,N.A. and Lawler,J.
Characterization of human and mouse cartilage oligomeric matrix
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Human germline oligomeric matrix protein (COMP) mRNA,
L32137
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germline; matrix protein.
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26. .2299
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/db_xref="taxon:9606"
758 c 809 g 36
                                              /gene="COMP"
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Query Match:
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/db_xref="GI:602450"
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/rpt_type=tandem
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/rpt_tamily="thrombospondin type 3"
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DEKLREDE PQCRKDNCYTVPNSCQEDVDRDGIGDACDDALDGCVPNEKDNCEPVPN
DQRNTDEDKWGDACDNCRSQKNDDQKUTTDQDGRGDACDDDLDGDRIRNQDNCPRVPN
SQKDSDGDGIGDACDDCPOKSNPDQADVDHDFVGDACDSDQDQDGDGHQDSRDNCPT
VPNSAQEDSDHGGGDACDDDDDDDCPVBSRDNCPLVPNBQGEDACDCYDTVQDDF
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DBGLAVGYTAFNGVDFEGTFHNTTVTDDDYAGFIFGYQDSSFYVVNMKQMEQTYWQA
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RWFLQHRPQVGYIRVRFYEGPELVADSNVVLDTTMRGGRLGVFCFSQENIIWANLRYR
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Ygapop 10.0,
Fgapop 6.0,
Delop 6.0,
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ALIGNMENTS

RESULT 1 AAZ50497 AAZ50497 standard; DNA; 369 BP 23-MAY-2000 AAZ50497; (first entry)

KDEL receptor inhibitor-6 DNA

KDEL receptor inhibitor; heat shock protein; immune respo oligomerisation domain; neoplasia; sarcoma; lymphoma; leu melanoma; carcinoma; glioblastoma; astromytoma; oncogene; infectious disease; allergy; autoimmune disease; ss. Chimeric -Adenovirus E3. Homo sapiens. immune response; leukaemia;

Chimeric

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                                                                                                                                        Alignment Scores: Pred. No.:
                                                                                                                                                                                  The patent discloses the use of KDEL receptor inhibitor to promote secretion of proteins that are normally retained within the cell such as CC heat shock proteins by inhibiting KDEL receptor-mediated return of protein complexes to endoplasmic reticulum. This makes the secreted heat CC protein complexes to endoplasmic reticulum. This makes the secreted heat CC response to a target antigen. The inhibitor protein comprises several CC subunits where each subunit comprises an oligomerisation domain and has CC at its carboxy terminus a region which binds to a KDEL receptor. The CC target antigen may be associated with diseases including neoplasia such CC astromytoma, with defective tumour suppressor genes, oncogenes, CC infectious diseases, allergy or autoimmune diseases. The present CC sequence encodes KDEL receptor inhibitor comprising regions encoding a Ccleavable signal peptide; the oligomerisation domain of human cartilage coligomeric matrix protein (COMP) pentamerisation domain; a camel 1gG CC cloker domain and the carboxy-terminal sequence KDEL. The subsequence CC cDCC is an alteration of rat COMP which provides increased stability via
                                          US-09-696-872-23 (1-109) x AAZ50497 (1-369)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibitors of the KDEL receptor which comprises an oligomerization domain useful for promoting secretion of proteins which are normally retained within the cell
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The patent discloses the use of KDEL receptor inhibitor to promote secretion of proteins that are normally retained within the cell such as heat shock proteins by inhibiting KDEL receptor-mediated return of protein complexes to endoplasmic reticulum. This makes the secreted heat shock proteins more accessible to the immune system and improves immune response to a target antigen. The inhibitor protein comprises several subunits where each subunit comprises an oligomerisation domain and has at its carboxy terminus a region which binds to a KDEL receptor. The target antigen may be associated with diseases including neoplasia such as sarcoma, lymphona, leukemia, melanoma, carcinoma, glioblastoma and astromytoma, with defective tumour suppressor genes, oncogenes, infectious diseases, allergy or autoimmune diseases. The present sequence encodes KDEL receptor inhibitor comprising regions encoding a cleavable signal peptide; the oligomerisation domain of human thrombospondin 4 (TSP4) trimerisation domain; a camel IGG linker domain alteration of rat cartilage oligomeric matrix protein which provides increased stability via disulphide bonds.
KDEL receptor inhibitor; heat shock protein; immune response; oligomerisation domain; neoplasia; sarcoma; lymphoma; leukaem
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Chimeric -
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infectious disease; allergy; autoimmune disease; ss.
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98..222
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ProGluGlyThrGlySerSerGluLysAspGluLeu

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23-MAY-2000 AAZ50501;

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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inhibitors of the KDEL receptor which comprises an oligomerization domain useful for promoting secretion of proteins which are normally retained within the cell -
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 387
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The patent discloses the use of KDEL receptor inhibitor to promote CC secretion of proteins that are normally retained within the cell such as CC heat shock proteins by inhibiting KDEL receptor-mediated return of CC protein complexes to endoplasmic reticulum. This makes the secreted heat CC shock proteins more accessible to the immune system and improves immune CC response to a target antigen. The inhibitor protein comprises several CC subunits where each subunit comprises an oligomerisation domain and has CC at its carboxy terminus a region which binds to a KDEL receptor. The CC target antigen may be associated with diseases including neoplasia such CC as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and CC astromytoma, with defective tumour suppressor genes, oncogenes, CC infectious diseases, allergy or autoimmune diseases. The present CC sequence encodes KDEL receptor inhibitor comprising regions encoding a CC cleavable signal peptide; a myc-tag; an N-glycosylation sequence; the CC oligomerisation domain of rat cartilage oligomeric matrix protein CC (COMP); a camel IgG linker domain and the carboxy-terminal sequence CC increased stability via disulphide bonds.
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P-PSDB; AAY44967.
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Indels:
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lymphoma; leukaemia;
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Best Local Si
Query Match:
DB:
 RESULT 7
AAZ50496
ID AAZ5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The patent discloses the use of KDEL receptor inhibitor to promote CC secretion of proteins that are normally retained within the cell such as CC heat shock proteins by inhibiting KDEL receptor-mediated return of CC protein complexes to endoplasmic reticulum. This makes the secreted heat Shock proteins more accessible to the immune system and improves immune CC response to a target antigen. The inhibitor protein comprises several CC subunits where each subunit comprises an oligomerisation domain and has CC at its carboxy terminus a region which binds to a KDEL receptor. The CC target antigen may be associated with diseases including neoplasia such CC as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and CC astromytoma, with defective tumour suppressor genes, oncogenes, CC infectious diseases, allergy or autoimmune diseases. The present CC sequence encodes KDEL receptor inhibitor comprising regions encoding a CC cleavable signal peptide; the oligomerisation domain from rat cartilage CC oligomeric matrix protein; a camel IgC linker domain and the carboxy creating sequence KDEL. This is introduced into host cells by suitable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inhibitors of the KDEL receptor which domain useful for promoting secretion retained within the cell -
   23-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 387
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                                AAZ50496;
                                                           AAZ50496 standard; DNA; 369
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                                                                                                                                                                                                                                                                                                                   GlnAspValArgAspTrpLeuArgGlnGlnValArgGluIleThrPheLeuLysAsnThr
                                                                                                                                     ProGluGlyThrGlySerSerGluLysAspGluLeu 109
                                                                                                                                                                             CCGCAGCCGAAACCGCAGCCGCAGCCGCAGCCGAAACCGCAGCCGAAACCGGAA
                                                                                                                                                                                                ProGlnProLysProGlnProGlnProGlnProGlnProLysProGlnProLysProGln
                                                                                                                                                                                                                                       CAAGACGTGAGAGAGCTCTTGCGACAGCAGCTCAAGGAGTCACCTTCCTGAAGAATACG
                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuLeuAlaLeuAlaAlaValCysSerAlaAlaLysLysGlySerSerLeuGlyGlyAsp
                                                                                                                      CCGGAAGGTACCGGATCATCAGAAAAAGATGAGTTG
                                                                                                                                                                                                                                                                ValmetGluCysAspAlaCysGly-----
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                        -GACCTAGCCCCACAGATGCTTCGAGAACTCCAGGAGACTAATGCGGCGCTG
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Matches:
Conservative:
Mismatches:
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The patent discloses the use of KDEL receptor inhibitor to promote secretion of proteins that are normally retained within the cell such as the shock proteins by inhibiting KDEL receptor-mediated return of protein complexes to endoplasmic reticulum. This makes the secreted heat shock proteins more accessible to the immune system and improves immune response to a target antigen. The inhibitor protein comprises several subunits where each subunit comprises an oligomerisation domain and has at its carboxy terminus a region which binds to a KDEL receptor. The target antigen may be associated with diseases including neoplasia such as sacroma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and astromytoma, with defective tumour suppressor genes, oncogenes, infectious diseases, allergy or autoimmune diseases. The present sequence encodes KDEL receptor inhibitor comprising regions encoding a cleavable signal peptide; the oligomerisation domain of Xenopus thrombospondin 4 (TSP4) trimerisation and including an additional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric - Mus sp.
Chimeric - Xenopus
Chimeric - Camelus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KDEL receptor inhibitor; heat shock protein; immune response; oligomerisation domain; neoplasia; sarcoma; lymphoma; leukaemia; melanoma; carcinoma; glioblastoma; astromytoma; oncogene; infectious disease; allergy; autoimmune disease; ss.
Sequence 369
                           sub-sequence; a camel IgG linker domain and the carboxy-terminal sequence KDEL. The subsequence GDCC is an alteration of rat cartilage oligomeric matrix protein which provides increased stability via disulphide bonds.
                                                                                                                                                                                                                                                                                                         Disclosure;
                                                                                                                                                                                                                                                                                                                                      Inhibitors of the KDEL receptor which comprises an oligomerization domain useful for promoting secretion of proteins which are normally retained within the cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-FEB-2000.
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   B₽;
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"Camel IgG
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Alignment Scores: Pred. No.:

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Percent Similarity:
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ50495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
                                                                                                                                                                                                                                                                                                                KDEL receptor inhibitor; heat shock protein; immune response; Oligomerisation domain; neoplasia; sarcoma; lymphoma; leukaemia; melanoma; carcinoma; glioblastoma; astromytoma; oncogene; infectious disease; allergy; autoimmune disease; ss.
                                                                                                   misc_feature
                                                                                                                                     misc_feature
                                                                                                                                                                                                                                              CDS
         28-JUL-1999;
                                                                                                                                                                      mat_peptide
                                                                                                                                                                                                         sig_peptide
                                                                                                                                                                                                                                                                                           Chimeric -
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                               10-FEB-2000.
                                                       WO200006729-A1
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Camelus sp.
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         99WO-US17147
                                                                                                                                                                                                          /product=
                                                                                                   /note= "Mouse
235..306
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                                                                                                                                      /product= "Mature
97..234
                                                                                                                                                                        /note= "Derived 69 . . 336
                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                      /*tag=
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                                                                           note= "Camel IgG linker domain"
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79.41%
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Alignment Scores:
                                                                                                         shock proteins more accessible to the immune system and improves immune response to a target antigen. The inhibitor protein comprises several subunits where each subunit comprises an oligomerisation domain and has at its carboxy terminus a region which binds to a KDEL receptor. The target antigen may be associated with diseases including neoplasia such as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and astromytoma, with defective tumour suppressor genes, oncogenes, infectious diseases, allergy or autoimmune diseases. The present sequence encodes KDEL receptor inhibitor comprising regions encoding a cleavable signal peptide; the oligomerisation domain of mouse thrombospondin 3 (TSP3) trimerisation domain including an additional sub-sequence; a camel IgG linker domain and the carboxy-terminal sequence MDEL. The subsequence GDCC is an alteration of rat cartilage oligomeric
                                              Sequence 369 BP; 87 A; 103 C;
                                                                                                                                                                                                                                                                                                                                                                                                                            The patent discloses the use of KDEL receptor inhibitor to promote secretion of proteins that are normally retained within the cell such as heat shock proteins by inhibiting KDEL receptor-mediated return of protein complexes to endoplasmic reticulum. This makes the secreted heat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inhibitors of the KDEL receptor which comprises an oligomerization domain useful for promoting secretion of proteins which are normally retained within the cell
                                                                                          matrix protein which provides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 4; 87pp; English.
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Percent Similarity: Best Local Similarity: Query Match: 3.71e-23 345.50 76.47% 62.75% 59.16% 21 Conservative: Mismatches: Indels: Gaps:

Pred. No.:

Length: Matches:

369 64 14 21 3

US-09-696-872-23 (1-109) x AAZ50495 (1-369)

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AAZ50494 standard; DNA; 357

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The patent discloses the use of KDEL receptor inhibitor to promote CC secretion of proteins that are normally retained within the cell such as CC heat shock proteins by inhibiting KDEL receptor-mediated return of protein complexes to endoplasmic retriculum. This makes the secreted heat CC protein complexes to endoplasmic retriculum. This makes the secreted heat CC response to a target antigen. The inhibitor protein comprises several CC subunits where each subunit comprises an oligomerisation domain and has CC at its carboxy terminus a region which binds to a KDEL receptor. The CC target antigen may be associated with diseases including neoplasia such CC as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and CC carget antigen with defective tumour suppressor genes, oncogenes, CC infectious diseases, allergy or autoimmune diseases. The present CC sequence encodes KDEL receptor inhibitor comprising regions encoding a CC cleavable signal peptide; the oligomerisation domain of mouse CC thrombospondin 3 (TSPS) trimerisation domain; a camel IgG linker domain CC alteration of rat cartilage oligomeric matrix protein which provides increased erablite. The subsequence GDCC is an alteration of rat cartilage oligomeric matrix protein which provides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              shock proteins more accessible to the immune system and improves immune response to a target antigen. The inhibitor protein comprises several subunits where each subunit comprises an oligomerisation domain and has at its carboxy terminus a region which binds to a KDEL receptor. The target antigen may be associated with diseases including neoplasia such as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and astromytoma, with defective tumour suppressor genes, oncogenes, infectious diseases, allergy or autoimmune diseases. The present sequence encodes KDEL receptor inhibitor comprising regions encoding a cleavable signal peptide; the oligomerisation domain of human phospholamban (PLB) pentamerisation domain; a camel IgG linker domain and the carboxy-terminal sequence KDEL. The subsequence GDCC is an alteration of rat cartilage oligomeric matrix protein which provides concreased stability via disulphide bonds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The patent discloses the use of KDEL receptor inhibitor to promote secretion of proteins that are normally retained within the cell such as heat shock proteins by inhibiting KDEL receptor-mediated return of protein complexes to endoplasmic reticulum. This makes the secreted heat
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RESULT 11
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                              Percent Similarity:
Best Local Similarity:
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                                                                                         Alignment
                                                                                                                                                                                                                           New nucleic acids are described which encode a protein comprising the second and third type 1 repeats of human TSP (thrombospondin)-1, but not the TGF (transforming growth factor)-beta activation region of human TSP-1. The nucleic acid of TSP (thrombospondin)-1 containing the second and third type-1 repeats and the COMP (cartilage oligomeric matrix protein) assembly sequence (COMP/TSP-1) was produced by PCR (polymerase chain reaction). Expression of COMP/TSP-1 caused inhibition of the growth of tumours in mice models. Thus the nucleic acids and proteins may be useful for treating angiogenesis related diseases such as cancer (by reducing the rate of growth and size of tumours), arthritis, psoriasis, diabetic retinopathy, corneal graft rejection, and glacoma. They may also be
                                                                                                                                                  used for treating human immunodeficiency virus (HIV) infection. Anti-angiogenic therapy has little toxicity, does not require the therapeutic agent to enter tumour cells or cross the blood-brain barrier, controls tumour growth independently of growth of tumour cell heterogeneity, and does not induce drug resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding chimeric proteins such as cartilage oligomeric matrix protein (COMP)/thrombospondins (TSP)-1 and 2, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thrombospondin; angiogenesis; tumour; treatment; cancer; arthritis; psoriasis; diabetic retinopathy; corneal graft rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA47734 standard; DNA; 755
                                                                                                                      Sequence 755
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Fig 4a-b; 40pp; English.
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Query Match: DB:

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                      New nucleic acids are described which encode a protein comprising the second and third type 1 repeats of human TSP (thrombospondin)-1, but not the TGF (transforming growth factor)-beta activation region of human TSP-1. The nucleic acid of TSP (thrombospondin)-1 containing the second and third type-1 repeats and the COMP (cartilage oligomeric matrix protein) assembly sequence (COMP/TSP-1) was
                                                                                                                                                                                                                                                                         Nucleic acids encoding chimeric proteins such as cartilage oligomeric matrix protein (COMP)/thrombospondins (TSP)-1 and 2, useful for inhibiting angiogenesis and treating diseases such as cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSP-1; TSP-2; COMP; cartilage oligomeric matrix protein; thrombospondin; angiogenesis; tumour; treatment; cancer; arthritis; psoriasis; diabetic retinopathy; corneal graf
                                                                                                                                                                                                                     Claim 44; Fig 5a-b; 40pp; English.
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25-APR-2001; :
23-MAY-2001; :
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                                                                                                               GENE LOGIC INC
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                                                      Nation M,
                                                                                                                                                                  ; 2001US-263757P.
; 2001US-286090P.
; 2001US-292517P.
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                                                         Diggans
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cancer;

differential expression;

ID NO:

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caused inhibition of the growth of tumours in mice models. Thus the nucleic acids and proteins may be useful for treating angiogenesis related diseases such as cancer (by reducing the rate growth and size of tumours), arthritis, psoriasis, diabetic retinopathy, corneal graft rejection, and glaucoma. They may also used for treating human immunodeficiency virus (HIV) infection. Anti-angiogenic therapy has little toxicity, does not require the therapeutic agent to enter tumour cells or cross the blood-brain barrier, controls tumour growth independently of growth of tumour cell heterogeneity, and does not induce drug resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 925 BP; 156 A; 310 C; 312 G; 147 T; 0 other;
                                                                                                                                                                                                                                                                               ValMetGluCysAspAlaCysGlyProGlnProGlnProLysProGlnProGlnProGln
                                                                                                                                                                                                                                                                                                                                          CAGGACGTGCGGGACTGCCGGCAGCAGGTCAGGGAGATCACGTTCCTGAAAAAACACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diagnosing breast cancer in a patient comprises detecting the level of gene expression in cell or tissue samples, where a differential gene expression is indicative of breast cancer -
                                                                                                                                         Breast cancer-associated gene sequence
                                                                                                                                                                              14-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                              Unidentified
                                                                                                                                                                                                                                             ABT07751 standard; DNA; 2439
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                                                                                           development;
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                                                                                                         ds; breast cancer; breast cancer-associated gene sequence;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention relates to methods of diagnosing breast lch comprise detecting the level of expression in a
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02-FEB-2001; 2001US-265928P.
09-APR-2001; 2001US-282698P.
09-APR-2001; 2001US-0829472.
04-MAY-2001; 2001US-288590P.
29-MAY-2001; 2001US-294443P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detecting a breast cancer-associated transcript in a patient's cell, useful for diagnosing breast cancer, comprises contacting a biological sample with a polynucleotide that selectively hybridizes with breast cancer nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2439
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                                                       ValMetGluCysAspAlaCysGlyProGlnProGlnProLysProGlnProGlnProGln ::: :::||| :::
                                                                                                                      GlnAspValArgAspTrpLeuArgGlnGlnValArgGluIleThrPheLeuLysAsnThr
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   ProGlnProLysPro
                                                                                                   CAGGACGTGCGGGACTGCCGGCAGCAGGTCAGGGAGATCACGTTCCTGAAAAAACACG
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                                   GTGATGGAGTGTGACGCGTGCGGGATGCAGCAGTCAGTACGCAC-CGGCCTACCCAGCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP;
                                                                                                                                                                   -TCAGACCTGGGCCCGCAGATGCTTCGGGAACTGCAGGAAACCAACGCGGCGCTG
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28-SEP-2000

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28-SEP-2000;
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27-SEP-2000;
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20-SEP-2000;
22-SEP-2000;
22-SEP-2000;
25-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid; stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                        Young PE,
Soppet DR,
        ,WPI; 2002-188264/24
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27-SEP-2000;
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25-SEP-2000;
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                                                   AVALON PHARM.
                        Augustus M, Weaver Z;
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2000US-235720P.
2000US-235863P.
2000US-236028P.
2000US-236034P.
2000US-236034P.
2000US-236111P.
2000US-236111P.
2000US-236111P.
2000US-236911P.
2000US-2379173P.
2000US-237914P.
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2000US-235077P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a method (M1) for screening for an CC anti-neoplastic agent. The method involves exposing cells to a chemical CC agent to be tested for anti-neoplastic activity, determining a change in CC expression of at least one gene (I) of a signature gene set, where (I) CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664 CC to ABL70110), or is at least 95% identical to (S), where a change in CC expression is indicative of anti-neoplastic activity. (I) has cytostatic CC activity and can be used in gene therapy. M1 can be used for screening CC is the data collected with respect to the anti-neoplastic agent as a CC result of M1, and the data is sufficient to convey the chemical CC treatment of cancer such as colon, breast, stome, thyroid, CC ossophageal, ovarian, kidney, prostate or pancreatic cancer, cafenoarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine CC carcinoma, papillary carcinoma and Wilm's tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene
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GCGGCCCCTGCTCCA
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                               ProGlnProLysPro
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-DB=18sued_Patents_NA -QPMT=fastap_-SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09696872 @CGN 1 1 76 @runat_26082003 151138 3255 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPEXT=0 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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-MODEL=frame+_p2n.model
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

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Copyright (c) 1993 - 2003 Compugen Ltd.
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GENERAL INFORMATION:
APPLICANT: Rothman, James
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31468
CURRENT APPLICATION UNMER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 30
LENGTH: 372
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                TCATTTTTGCGAAACACCATAGCTGAATGCCAGGCTTGCGGTCCGCAGCCGCAGCCGAAA 255
                                                                                                                                        CAATTAAACCAACTCCTGGGAGAGGTGAAGGACCTTCTGAGACAGCAGGTTAAGGAAACA 195
                                                                                                                                                            GluThrAsnAlaAlaLeuGlnAspValArgAspTrpLeuArgGlnGlnValArgGluIle 61
                                                                                                                                                                                                                 SerSerLeuGlyGlyAspCysSerAspLeuGlyProGlnMetLeuArgGluLeuGln 41
                                                                                                                                                                                                                                                                     ArgTyrMetIleLeuGlyLeuLeuAlaLeuAlaAlaValCysSerAlaAlaLysLysGly 21
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77.78%
78.60%
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Conservative:
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Indels:
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US-09-124-671-16
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US-09-124-671-28
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Sequence 16, Application US/09124671A
Patent No. 6166088
GENERAL INFORMATION:
APPLICANT: Rothman, James
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FASTSEQ for Windows Version 3.0
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Best Local Similarity:
Query Match:
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CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FASTSBQ for Windows Version 3.0
SEQ ID NO 28
LENGTH: 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rothman, James
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
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72.22%
73.46%
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Conservative:
Mismatches:
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Percent Similarity:
Best Local Similarity:
Query Match:
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DB:
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; OTHER INFORMATION: chimeric rat
US-09-124-671-16
                                                                                    Score:
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US-09-124-671-35
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Best Local Similarity:
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US-09-696-872-23 (1-109) x US-09-124-671-35 (1-444)
                                                                                                  Pred. No.:
                                                                                                              Alignment Scores:
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                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: ROCLMMAN, James
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 16
LENGTH: 387
                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/124,671A CURRENT FILING DATE: 1998-07-29 NUMBER OF SEQ ID NOS: 42 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 35 LENGTH: 444
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 35, Application US/09124671A Patent No. 6160088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           319 CCGGAAGGTACCGGATCATCAGAAAAAGATGAGTTG
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80.36%
77.68%
73.37%
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422.00
84.85%
82.83%
72.26%
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Matches:
Conservative:
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Matches:
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Sequence 14, Application US/09124671A

Patent No. 616008

GENERAL INFORMATION:

APPLICANT: Rothman, James

APPLICANT: Hoe, Mee

APPLICANT: Hoe, Mee

TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS

FILE REFERENCE: 31488

CURRENT APPLICATION NUMBER: US/09/124,671A

CURRENT FILING DATE: 1998-07-29

NUMBER OF SEQ ID NOS: 42

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 14

LENGTH: 387

TYPE: DNA

ORGANISM. Artificial Common
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Best Local Similarity:
Query Match:
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; OTHER INFORMATION: chimeric rat COMP-KDEL
US-09-124-671-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 GlySerSerLeuGlyGlyAspCysCysSerAspLeuGlyProGlnMetLeuArgGluLeu
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                                                                                                                                             48 GlnAspValArgAspTrpLeuArgGlnGlnValArgGluIleThrPheLeuLysAsnThr
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                                                                                                                                                                                                                                                            40 Trecrecrecrecececere
                                                                                                                                                                                                                                                                               8 LeuLeuAlaLeuAlaAlaValCysSerAlaAlaLysLysGlySerSerLeuGlyGlyAsp
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                                                                                ValMetGluCysAspAlaCysGly------ProGln
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               ProGlnProLysProGlnProGlnProGlnProGlnProLysProGlnProLysProGlu
                                                                                                                            CAAGACGTGAGAGAGCTCTTGCGACAGCAGGTCAAGGAGATCACCTTCCTGAAGAATACG
                                                           GTGATGGAATGTGACGCTTGCGGAATGCAGCCCGCACCCCCCGGTACTAGTCCGCAG
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414.50
79.46%
76.79%
70.98%
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Matches:
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GENERAL INFORMATION:
APPLICANT: ROTHMAN, James
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
CURRENT APPLICATION UNUBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 22
LENGTH: 369
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
CTHER INFORMATION Chimals Transport Control of the c
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US-09-124-671-22
; Sequence 22, Ap
; Patent No. 6160
GENERAL INFORMATION:
APPLICANT: Rothman, James
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
                                                                                                                                                                                                                                                                  US-09-124-671-20
; Sequence 20, Application
; Patent No. 6160088
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Best Local Similarity:
Query Match:
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GENERAL INFORMATION:
APPLICANT: Rothman, James
APPLICANT: Rothman, James
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 3148
CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 18
LENGTH: 357
TYPE: DNA
ORGANIEM: Artificial Sequence
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; ORGANISM: Artificial Sequence; FEATURE;
; OTHER INFORMATION: chimeric m
US-09-124-671-20
           Best Local Similarity:
Query Match:
                                         Percent Similarity:
                                                      Score:
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                                                                                                              ; OTHER INFORMATION: US-09-124-671-18
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Pred. No.:
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SEQ ID NO 20
LENGTH: 369
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Patent No. 6160088
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GENERAL INFORMATION:
APPLICANT: Rothman, James
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
CURRENT FILLING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
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LENGTH: 315
TYPE: DNA
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                                                                                                                                                  GluThrAsnAlaAlaLeuGlnAspVal-----ArgAsp-TrpLeuArgGlnGlnValAr 59
                                                                                                                                                                                                        TCCAGCCTGGGTGGAGACTGTTGTCAAAAGCTACA-GAATCTATTTATCAATTTCTGTCT
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                                                gGluIleThrPheLeuLysAsnThrValMetGluCysAspAlaCysGlyProGlnProGl 79
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Matches:
Conservative:
Mismatches:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: FMS-DOS Version
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION NDATA:
APPLICATION NUMBER: PCT/US93/117;
FILING DATE: filed herewith
PRIOR APPLICATION NUMBER: 07/985,296
FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: GATES, Edward R.
REGISTRATION NUMBER: 31,616
REGISTRATION NUMBER: 31,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield,
STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
TITLE OF INVENTION:
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COUNTRY: United States of America
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859 GCTCCC---CCTGCACCGCCAACACGCCCA 885
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                                           87 GlnProGlnProLysProGlnProLysPro
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                                                                                                                                                                                                                                         51 ArgAspTrpLeuArgGlnGlnValArgGluIleThrPheLeuLysAsnThrValMetGlu 70
                                                                                                                                                                                                                                                                                                                                                                31 AspLeuGlyProGlnMetLeuArgGluLeuGlnGluThrAsnAlaAlaLeuGlnAspVal
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; MOLECULE TYPE: CDNA
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Xenopus laevis
; ORGANISM: Xenopus laevis
; DEVELOPMENTAL STAGE: Stage
PCT-US93-11725-1
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PCT-US93-11725-1
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: filed herewith
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 0/985,294
FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: GATES, Edward R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: B0801
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2820 base pairs
TYPE: nucleic acid
CTP.NUTCHARCTERIST
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/U
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MEDIUM TYPE: Diskett
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield, & Sacke,
STREET: 600 Atlantic Avenue
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                                                                     604
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                                                                                                                                                                                                                                                                                        PheLeuLysAsnThrValMetGluCysAspAlaCysGlyProGlnProGln---ProLys 81
                                                                                                                                                                                                                                         ThrAsnAlaAlaLeuGlnAspValArgAspTrpLeuArgGlnGlnValArgGluIleThr 62
                                                                                                                                                                                                                                                                                                                        SerLeuGlyGlyAspCysCysSerAspLeuGlyProGlnMetLeuArgGluLeuGlnGlu 42
ACTTCATGTTTCAGAGGAGTGCGGTGCATTGATACAGAGGGCGGCTTCCAATGTGGGCCG 723
                                                                   CCAACCAAAGTTCCCCAGCGCCTAGCCACCACTACACCTCCAAAGCCTCGATGTGATGCA 663
                                                                                                       ProGlnProGlnProGln------ProGlnProLysPro------
                                                                                                                                             TTCTTGAGAAACACCATTGCAGAATGCCAGGCCTGTGGCTTAGGTCCTGACTTCCCATTG 603
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IBM-compatible
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Matches:
Conservative:
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Indels:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-643-597-324
US-09-480-884A-324
                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Hosken, Nancy A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C6
                                                 CURRENT APPLICATION NUMBER: US/09/480,884A
CURRENT FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 330
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 324
LENGTH: 521
                                                                                                                                                                                                                                                                                                                           Sequence 324, Application US/09480884A Patent No. 6482597 GENERAL INFORMATION:
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SEQ ID NO 324
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APPLICANT: MCNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
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               TYPE: DNA
ORGANISM: Homo sapien
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Skeiky, Yasir A.W.
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Hosken, Nancy
Fanger, Gary R.
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APPLICANT: Wang, Tongtong
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Hosken, Mancy A.
APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy A.
APPLICANT: Franger, Garry R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSEQ for Windows Version 3.0
SSOFTWARE: FastSEQ for Windows Version 3.0
SSOFTWARE: FastSEQ for Windows Version 3.0
SSOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
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Query Match:
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Search completed: August 26, 2003, 19:22:49 Job time : 87.8496 secs
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249 CCTCAGCCCCAG 260
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249 CCTCAGCCCCAG 260
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Perfect score:
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1: /cgn2_6/ptodata/1/pubpna/US07
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ALIGNMENTS

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US-09-919-603-4

(Sequence 4, Application US/09919603

Patent No. US20020137679A1

GENERAL INFORMATION:

GENERAL INFORMATION: COMP/TSP-2 and Other TSP

TITLE OF INVENTION: COMP/TSP-1, COMP/TSP-2 and Other TSP

TITLE OF INVENTION: Chimeric Proteins

FILE REFERENCE: 1440-1033-007

CURRENT APPLICATION NUMBER: US/09/919,603

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: PCT/US00/02482

PRIOR APPLICATION NUMBER: 60/118,053

PRIOR FILING DATE: 1999-02-01

NUMBER OF SEQ ID NOS: 21

SOPTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4

LENCTH: 755

TYPE: DNA

OTHER INFORMATION: fusion gene

US-09-919-603-4
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262.5

44.9

755 10 US-09-919-603-4

Sequence 4, Appli

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APPLICANT: Lawler, John W.

TITLE OF INVENTION: COMP/TSP-1, COMP/TSP-2 and Other TITLE OF INVENTION: COMP/TSP-1, COMP/TSP-2 and Other TITLE OF INVENTION: Chimeric Proteins

FILE REFERENCE: 1440.103-007

CURRENT APPLICATION NUMBER: US/09/919,603

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: PCT/US00/02482

PRIOR FILING DATE: 2000-02-01

PRIOR FILING DATE: 1999-02-01

PRIOR FILING DATE: 1999-02-01

NUMBER OF SEO ID NOS: 21

SOFTWARE: FASTSEQ for Windows Version 4.0

SEO ID NO 6

SEO ID NO 6
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                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: fusion
                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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                  CysCysSerAspLeuGlyProGlnMetLeuArgGluLeuGlnGluThrAsnAlaAlaLeu 47
                                                             CIGCTCACCCIGGCTGCCCTCGGCGGCGTCCGGACAGGCCCAGAGCCCGTTGGGC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CysCysSerAspLeuGlyProGlnMetLeuArgGluLeuGlnGluThrAsnAlaAlaLeu 47
                                                                               LeuLeuAlaLeuAlaAlaValCysSerAlaAlaLysLysGlySerSerLeuGlyGlyAsp 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGCTCACCCTGGCTCCGCCGCGCGCGCCGACAGGCCCAGAGCCCGTTGGGC-----
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TCAGACCTGGGCCCGCAGATGCTTCGGGAACTGCAGGAAACCAACGCGGCGCTG 160
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PRIOR APPLICATION NUMBER: US/60/233,133
PRIOR FILING DATE: 2000-09-16
PRIOR PELLING DATE: 2000-09-20
PRIOR PELLING DATE: 2000-09-20
PRIOR PELLING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,034
PRIOR APPLICATION NUMBER: US/60/234,509
PRIOR APPLICATION NUMBER: US/60/234,509
PRIOR APPLICATION NUMBER: US/60/234,567
PRIOR PILING DATE: 2000-09-22
PRIOR PILING DATE: 2000-09-22
PRIOR PILING DATE: 2000-09-22
PRIOR PILING DATE: 2000-09-22
NUMBER OF SEO ID NOS: 1392
SOFTWARE: PALENTIN VERSION 3.0
SEQ ID NO 140
LENGTH: 2439
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US-09-954-531-140
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US-09-954-531-359
                 RESULT
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores: Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 140, Application US/09954531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Process for Identifying TITLE OF INVENTION: Gene Sets FILE REFERENCE: 689290-77 CURRENT APPLICATION NUMBER: US/09/954,531 CURRENT FILING DATE: 2002-05-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo
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                                                GCGGCCCCTGCTCCA
                                                                              ProGlnProLysPro 92
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Patent No.

359, Application US/09954531 o. US20020165180A1

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Best Local Similarity:
Query Match:
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; ORGANISM: Homo sapiens
US-09-954-531-359
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SEQ ID NO 359
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                                                            CURRENT APPLICATION NUMBER: US/09/918,624B
CURRENT FILING DATE: 2002-12-03
PRIOR APPLICATION NUMBER: 60/222,470
PRIOR FILING DATE: 2000-07-28
                                                                                                                                                APPLICANT: Schebye, Xiao Min
APPLICANT: Sornasse, Thierry
TITLE OF INVENTION: CDMSE EXPRESSED IN ADIPOCYTE
FILE REFERENCE: PA-0033 US
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PRIOR FILING DATE: 2000-09-20
PRIOR PPLICATION NUMBER: US/60/234,509
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US/60/234,567
PRIOR FILING DATE: 2000-09-22
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                  NUMBER OF SEQ ID NOS: 71
SOFTWARE: PERL Program
SOFTWARE: PIEQ ID NO 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 1392
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APPLICATION NUMBER: US/60/233,133
FILING DATE: 2000-09-18
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Best Local Similarity:
NAME/KEY: CDS
; LOCATION: (26)...(2299)
US-10-301-822-40
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                                                                                                                           SOFTWARE: FO
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Publication No.
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APPLICANT:
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TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MPMO1-029P2RNM
                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/381,988 PRIOR FILING DATE: 2002-05-20
                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/301,822
CURRENT FILING DATE: 2002-11-21
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                                                                        TYPE: DNA
ORGANISM: Homo
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OTHER INFORMATION: GenBank ID No. US20030113720A1 g602449
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Monahan, John E.
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No. US20030148410A1
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Matches:
Conservative:
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APPLICANT: PUBZEA; LAjos
APPLICANT: Meric, Funda
APPLICANT: Meric, Funda
APPLICANT: Sahin, Aysegul
APPLICANT: Mills, Gordon B.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-038
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 60/299,887
PRIOR APPLICATION NUMBER: US 60/301,572
PRIOR APPLICATION NUMBER: US 60/301,572
PRIOR APPLICATION NUMBER: US 60/306,501
PRIOR APPLICATION NUMBER: US 60/306,501
PRIOR APPLICATION NUMBER: US 60/306,501
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: US 60/325,002
PRIOR FILING DATE: 2001-09-25
PRIOR PILING DATE: 2001-09-25
PRIOR PILING DATE: 2001-09-25
PRIOR PILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/362,585
PRIOR APPLICATION NUMBER: US 60/362,585
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-696-872-23 (1-109) x US-10-301-822-40
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Publication No. US20030124128A1
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APPLICATION NUMBER: US 60/xxx,xxx
FILING DATE: 2002-05-14
R OF SEQ ID NOS: 506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGGACGTGCGGGACTGGGCTGCGGCAGCAGGTCAGGGAGATCACGTTCCTGAAAAACACG
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Hoersch, Sebastian
Monahan, John
Meyers, Rachel E.
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Kamatkar, Shubhangi
Mertens, Maureen
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bbagyi, Gabriel
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Gaps:
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Matches:
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; LENGTH: 2439
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-177-293-71
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US-10-154-971-21
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21, Application US/10154971 Publication No. US20030088074A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/945,244
PILING DATE: <Unknown>
APPLICATION NUMBER: PCTEP96/01725
APPLICATION NUMBER: PCTEP96/01725
FILING DATE: 25-APR-1996
APPLICATION NUMBER: EP 95400932.0
FILING DATE: 25-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: GOLLIn, Michael A.
REGISTRATION NUMBER: 31,957
REFERENCE/DOCKET NUMBER: GUPLA 0003
                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/154,971
FILING DATE: 28-May-2002
                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: VARIABLE FRAGMENTS OF IMMUNOGLOBULINS
USE FOR THERAPEUTIC OR VETERINARY PURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENCER & FRANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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Matches:
Conservative:
Mismatches:
Indels:
     GUPLA 0003
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TELECOMMUNICATION INFORMATION:

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RESULT 9
US-10-154-971-23
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Best Local Similarity:
Query Match:
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TELEFAX: 202-414-4040
INFORMATION FOR SEQ ID NO: 21:
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/154,971

FILING DATE: 28-May-2002

CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/945,244

FILING DATE: <UNKNOWN>
APPLICATION NUMBER: PCT/EP96/01725

FILING DATE: 25-APR-1996

APPLICATION NUMBER: EP 95400932.0

FILING DATE: 25-APR-1995

ATTORNEY/AGENT INFORMATION:

NAME: GOllin, Michael A.

REGISTRATION NUMBER: 31,957

REFERENCE/DOCKET NUMBER: GUPLA 0003

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENCER & FRANK
STREET: 1100 New York Avenue, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: VARIABLE FRAGMENTS OF IMMUNOGLOBULINS -
TITLE OF INVENTION: VARIABLE FRAGMENTS OF VETERINARY PURPOSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 537 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20005
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 20005
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LOCATION: 1...
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Indels:
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Matches:
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APPLICANT: Meagher, Madeleine
APPLICANT: Xu, Jiangchun
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.504
CURRENT APPLICATION UNUMBER: US/09/815,343
CURRENT APPLICATION UNUMBER: US/09/815,343
CURRENT FILING DATE: 2001-03-22
INUMBER OF SEQ ID NOS: 1556
SOFTWARE: Fast(SEQ for Windows Version 4.0
SEQ ID NO 1091
LENGTH: 320
                                                                                                                                                                                                                                                                  ; TYPE: DNA
; OTGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(320)
; OTHER INFORMATION: n = A,T,C or
US-09-815-343-1091
                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
                                                                                                           US-09-696-872-23 (1-109) x US-09-815-343-1091 (1-320)
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                                                                                                                                                                                                                                   Alignment Scores:
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RMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
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SEQUENCE DESCRIPTION: SEQ
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96 ProGluPro 98
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                                                  60 GÁCTTTAACCGGCÁGTTCTTGGGTCAAATGACACAATTAAACCAACTCCTGGGAGAGGTG 119
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                             AspLeuGlyProGlnMetLeuArgGluLeuGlnGluThrAsnAlaAlaLeuGlnAspVal 50
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Matches:
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DB:
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ORGANISM: Streptomyces avermitilis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1734)
US-10-156-761-4994
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US-10-156-761-4994
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
Pred. No.:
              APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORITAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLECTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR PRIOR FILING DATE: 2001-05-97
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                               Sequence 1, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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Publication No. US20030119018A1
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
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NUMBER: US/10/156,761
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wang, Aijun

APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.

APPLICANT: Fanger, Neil

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C14

CURRENT APPLICATION NUMBER: US/09/735,705

CURRENT FILING DATE: 2000-12-12

INUMBER OF SEQ ID NOS: 419

SOFTWARE: FastSEQ for Window-

SEQ ID NO 324

LENGTH: 521

TYPE: DW*
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US-09-735-705-324
US-09-696-872-23 (1-109) x US-09-735-705-324 (1-521)
                                              Query Match:
                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                  Pred. No.:
                                                                                                                                Alignment Scores:
                                                                                                                                                                  ) ORGANISM: Homo sapien US-09-735-705-324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-696-872-23 (1-109) x US-10-156-761-1 (1-9025608)
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Best Local Similarity:
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PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. Use.
Patent No. Use.

Patent No. Use.

Patent No. Use.

Patent No. Use.

Patent No. Use.
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NAME/KEY: misc_feature
LOCATION: (4187715)
OTHER INFORMATION: a, t
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Fan, Liqun
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APPLICANT: Fanger, Gary R.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Veatter, Darrick

APPLICANT: Watanabe, Yoshihiro

APPLICANT: Watanabe, Yoshihiro

APPLICANT: Henderson, Robert A.

APPLICANT: Peckham, David W.

APPLICANT: Fanger, Neil

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C16

CURRENT APPLICATION NUMBER: US/09/897,778

CURRENT APPLICATION NUMBER: US/09/897,778

CURRENT FILING DATE: 2001-06-28

NUMBER OF SEQ ID NOS: 467

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 324
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                            APPLICANT: Wang, Tongtong
APPLICANT: Marnerakis, Mar
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas
APPLICANT: Carter, Darrick
APPLICANT: Watanabe, Yoshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: KALOS, MICHAEL D.
APPLICANT: MCNEILI, PALTICIA D.
APPLICANT: RETES, MAZE W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 324
LENGTH: 521
TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 324, Application US/09897778 Patent No. US20020147143A1
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TYPE: DNA
ORGANISM: Homo sapiens
                                              ENGTH: 521
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249 CCTCAGCCCCAG 260
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249 CCTCAGCCCCAG 260
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                                                                                                                                                                                                                     Alignment Scores:
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249 CCTCAGCCCCAG 260
                                                      189 CCTCAGCCTCAGCCGCAACCCCAAGCCCCAATCACAACCCCAGCCTCAGCCCCAACCCAAG 248
                        96 ProGluProGlu 99
                                                                        76 ProGlnProGlnProLysProGlnProGlnProGlnProGlnProLysProGlnProLys
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20.89%
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Matches:
Conservative:
Mismatches:
Indels:
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Search completed: August 26, 2003, 21:02:49 Job time: 1541.5 secs

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Copyright
GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
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Command line parameters:

-MODEL-frame+ p2n.model -DEV=xlh
-MODEL-frame+ p2n.model -DEV=xlh
-Q-/cgn2 _1/USPTO_spool/US08696872/runat _26082003_151137_3236/app_query.fasta_1.462
-DB=EST -QFMT=fastap -SUFFIX=xst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=50 -MINLEN=0 -MAXLEN=200000000
-USER=US0969872 @CGN 1 1 3596 @runat 26082003 151137 3236 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MĀIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOD=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
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Maximum DB seq length: 2000000000
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Ygapop 10.0,
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       22781392 seqs, 12152238056 residues
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em_estom: *
em_gss_hum: *
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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ORGANISM	KEYWORDS SOURCE	VERSION	DEFINITION	RESULT 1 BE809033		ij	44	43	41	40	ယ ယ တ ထ	37	J G	34	33	3 1 1	30	2 2 9 8	27	26	226	23	221	20	18	17	15	14	ر د د د	11	10	00	7 6	σ,	Ŀω	NI		Result No.
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Chordata, Craniata, Verte Cetartiodactyla, Ruminant		.45	518 bp mRNA taurus cDNA 5', mRNA		ALIGNMENTS	-	5 55	82	83	BG899861*	BG998353	AW067829	BG898451	BG85	BG898326	689	G85	G 85	BG900465	BG89/511	8 8	BG900459	BG896503	BG898382	BG896332 BG900343	BG898027	AW068338 BG900556	BG896387	BG898406 BG899727	BG897214	BG897326	BG89	BY335264 BG900764		CB712965 BG900312	612	BE809033	ID
Vertebrata; Euteleostomi; inantia; Pecora; Bovoidea;			innear EST 25-APR-2001 sequence.			SOLOLY WORDS-1-	896555 HOA47-1-	99824 HOA40-	898320 HOA55-1- 897459 HOA13-1-	899861 HOA40-1-	98353 HOA55-1- 00134 HOA51-1-	cn19f09.x	- HOA9	HOA5	HOA5	HOA4	нод3	HOA1		HOA2	HOA1:	HOA4	HOA3	HOA8	HOA2	HOA2	Cn20g	HOA30-1-	HOAS	нолз:	HOA12-1-	HOA2	HOA4	BY350582	CB712965 AMGNNUC:T	AV612410	P 1	Description

BEROSORI I	
LOCUS	BE809033 518 bp mRNA linear EST 25-APR-2001
DEFINITION	214373 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION	BE809033
VERSION	BE809033.1 GI:10240145
KEYWORDS	EST.
SOURCE	Bos taurus (cow)
ORGANISM	Bos taurus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
	Bovidae; Bovinae; Bos.
REFERENCE	1 (bases 1 to 518)

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Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Therenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegraid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
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                                                                                                                                                      GTGATGGAGTGTGACGCGTGCGGGATGCAACCCGCGAACCCCCAAACTGACGGTACGG 286
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                                                                                   CCGCTAAGCCAGTGTTCGCCCGGCTTCTGCTTCCCCGGAGTGGCTTGTACCGAGACAGCC 346
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/mol_type="mRNA"
/mb xref="taxon:9913"
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/clone_lib="WARC 2BOV"
/clone="vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
/note="vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
/ibrary made from pooled tissue from testis, thymus,
semitendonosus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."
85 a 187 c 160 g 86 t
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This clone was obtained from a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fuk
Tel: 81-248-25-5641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bovine ESTs
Nucleic Acids Res. 29 (22), E108 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Establishment of a high throughput EST sequencing system using poly(A) tail-removed cDNA libraries and determination of 36,000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Yoshikazu Sugimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Takasuga, A., Hirotsune, S., Itoh, R., Jitohzono, A.,
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
ProGlnProLysProGlnPro----
                                   GTGATGGAGTGTGACGCGTGCGGGATGCAACCCGCGCGAACCCCCAAACTGACGGTACGG
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                                                                                                                                                                                                 CysCysSerAspLeuGlyProGlnMetLeuArgGluLeuGlnGluThrAsnAlaAlaLeu
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/tissue_type="lung"
/dev_stage="fetus"
/lab_host="DH10B"
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/note="Vector: pZL1; Site_1: Sal1;
was deleted from a Not1 site"
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|mol_type="mRNA"
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Bos taurus cDNA clone E1LU045D06 5',
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3 others

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Not1;

CDNA

961-8061,

Suzuki, H., Aso, H.

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AUTHORS
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                       Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                     No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                 202
                            322
                                                                                     262
                                                                                                                                                                                                           151
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                                                      88
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                                                                                                                                                                                                                                                                    94
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AMGNNUC:TRGS2-00012-H5-A trgs2 (10306)
trgs2-00012-h5 5', mRNA sequence.
CB712965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 805 447-4881
Plate: 00012 row: h column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 496)
Amgen EST Program.
Amgen Rat EST Program
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Norway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CB712965.1 GI:29770113
                                                                                                     ValMetGluCysAspAlaCysGlyProGlnProGlnProLysProGlnProGlnProGln :::
                                                                                                                                                                GlnAspValArgAspTrpLeuArgGlnGlnValArgGluIleThrPheLeuLysAsnThr 67
                                                                                                                                                                                                           -----GACCTAGCCCCACAGATGCTTCGAGAACTCCAGGAGACTAATGCGGCGCTG
                                                                                                                                                                                                                                                                   GTGCTCGCCCTGGCTTGCGGGCTACCGGCCAGGGCCAGATCCCGCTGGGTGGA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACGGCGCGCGCTGCGGACCCTGCCCCGAAGGTTTCACAGGCAAC 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCGCTAAGCCAGTGTTCGCCCGGCTTCTGCTTCCCCGGAGTGGCTTGTACCGAGACAGCC
                                                                                                                                              CAAGACGTGAGAGAGCTCTTGCGACAGCAGGTCAAGGAGTCACCTTCCTGAAGAATACG
                                                                                                                                                                                                                             CysCysSerAspLeuGlyProGlnMetLeuArgGluLeuGlnGluThrAsnAlaAlaLeu
                                                                                                                                                                                                                                                                                       LeuLeuAlaLeuAlaAlaValCysSerAlaAlaLysLysGlySerSerLeuGlyGlyAsp
:::||||||||||||||
                            CCAGTGCCGCTCTGCGCACCC 342
                                                        ProGlnProLysProGlnPro
                                                                                     Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10116"
/clone="trgs2-00012-h5"
/tissue type="muscle"
/clone_Tib="trgs2 (10306)"
/clone_Tib="trgs2 (10306)"
/note="Vector: C6KPGF7L; Site 1: Sall; Site_2: gastricnemius and soleus muscle"
gastricnemius and soleus muscle"
147 c 129 g 75 t 69 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dan Fitzpatrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                         6.94e-14
249.00
71.26%
63.22%
42.64%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   type="mRNA"
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Matches:
Conservative:
Mismatches:
Indels:
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Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ú
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA
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                                                                                                                                                                                                                                                                                                                                                            496
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REFERENCE
AUTHORS
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ORGANISM
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
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MEDLINE
PUBMED
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                                                                                                                                                                                                                                                     137
                                                             305
                                                                                                                           245
 364 GCGGCCCCTGCTCCACTGCGCGCCCCG
                                                                                                                                                                                       191 -----TCAGACCTGGGCCCGCAGATGCTTCGGGAACTGCAGGAAACCAACGCGGCGCTG
                                                                                           8
                                                                                                                                                        48
                                                                                                                                                                                                              28 CysCysSerAspLeuGlyProGlnMetLeuArgGluLeuGlnGluThrAsnAlaAlaLeu
                                                                                                                                                                                                                                                                        8 LeuLeuAlaLeuAlaAlaValCysSerAlaAlaLysLysGlySerSerLeuGlyGlyAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identification and initial characterization sequenced tags (ESTs) each from adult human osteoarthritic cartilage cDNA libraries Osteoarthr. Cartil. 9 (7), 641-653 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: sanjay_kumar-1@gsk.com
Seq primer: T7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 610-270-5598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            709 Swedeland Road,
Tel: 610-270-7245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlaxoSmithKline
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Ho. Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C.,
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BG900312.1 GI:14310561
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HOA37-1-C8 HOA (Human
                                                                                                                                             GlnAspValArgAspTrpLeuArgGlnGlnValArgGluIleThrPheLeuLysAsnThr
                                                                                                                             CAGGACGTGCGGGAGCTGCTGCGGCAGCAGGTCAGGGAGATCACGTTCCTGAAAAAACACG
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                                                                               ProGlnProLysProGlnProLysPro
                                                             GTGATGGAGTGTGACGCGTGCGGGATGCAGCAGTCAGTACGCAC-CGGCCTACCCAGCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="cartilage"
/lab_host="E.coli_DH10_B"
/clone_ib="HAA (Human Osteoarthritic Cartilage)"
/note="Vector: pSPORT I; Site_1: SalI; Site_2: Not
Directional"
a 212 c 171 g 85 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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73.03%
64.04%
42.64%
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RESULT

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337 bp mRNA linear BY350582 RIKEN full-length enriched, whole joints clone L830018K02 5', mRNA sequence.
encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN
Sciences Center (SSC), Yokohama Institute
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URL:http://genome.gsc.riken.go.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,
M., Maki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
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                                                                                                                                                                                                                                                                                                                                                                                                Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) RIKEN integrated sequence analysis (RISA) system--384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Okazaki, Y., Furuno, M.,
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                                                                                                                                                                                                                                                                                                              ng pipeline with 384 multicapillary sequencer. Genome 1757-1771 (2000)
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Okazaki, T., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Mikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Belsel, K. W., Blake, J. A., Bradt, D., Brusic, V., Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C.F. Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanaj, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, K. Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki
                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Tissues were provided by Vassilis Aidinis ( Biomedical Sciences Tissues were provided by Vassilis Aidinis ( Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari, Greece ) whose assistance we gratefully
                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlnAspValArgAspTrpLeuArgGlnGlnValArgGluIleThrPheLeuLysAsnThr
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RIKEN full-length enriched, synovial fib
cDNA clone L130042013 5', mRNA sequence.
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/clone_lib="RIKEN full-length enriched, whole joints"
108 c 108 g 58 t
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/mol_type="mRNA"
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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URL:http://genome.gsc.riken.go.jp,
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Nibata,K., Shiraki,T., Tagami, Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami, Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami, Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami, Sakazume,N., Sato,K., Shibata,K., Shiraki,T., Tagami, Sato,K., Shiraki,T., Shiraki,T., Shiraki,T., Tagami, Sato,K., Shiraki,T., Shiraki,
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tissues were provided by Vassilis Aidinis ( Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari,Greece ) whose assistance we gratefully
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Please visit our web site (http://genome.gsc.riken.go.jp)
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/db_xref="taxon:10090"
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5.92e-14
248.00
65.66%
58.59%
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Matches:
Conservative:
Mismatches:
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Miyazaki,A.
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Score:

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Best Local Similarity:
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                                                                                                            BASE COUNT
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                                                                                                                                                                                                                                                                                 Seq
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                                                                                                                                                                                                                                                                                                                    Fax: 610-270-5598
                                                                                                                                                                                                                                                                                                                                                                GlaxoSmithKline
                                                                                                                                                                                                                                                                                                                                                                                  UW2109
                                                                                                                                                                                                                                                                                                                                                                                              Contact: Sanjay Kumar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Sathe, G., Mui, P., Agarwal, P., Badger, A.M., Lee
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                 primer:
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                                                                                                                                                                                                                                                                                                sanjay
                                                                                                            Directional"
123 c
                                                                                                                                      /tissue_type="cartilage"
/lab_host="E.Coli DH10 B"
/clone_lib="HOA (Human Osteoarthritic Cartilage)"
/note="Vector: pSPORT I; Site_1: SalI; Site_2: No
                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                    Location/Qualifiers
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/db_xref="taxon:9606"
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302 67 242 47 188

EST 20-JUN-2002

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DB:
                    Percent Similarity:
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Sathe, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen,
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                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Sanjay Kumar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 350)
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BG897877.1 GI:14308126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG897877
                                                                                                                                                                                                                                                                                                       Email: sanjay_kumar-1@gsk.com
Seq_primer: T7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGGACGTGCGGGAGCTGCGGCAGCAGGTCAGGGAGATCACGTTCCTGAAAAAACACG
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                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9666"
/tissue_type="cartilage"
/lab_host="E_coli_DH10_B"
/clone_lib="HOA (Human Osteoarthritic Cartilage)"
/note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
Directional"
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1 (Dases 1 to 328)

Jia,L.B., Young,M.F., Touchman,J.W., Bouffard,G.G.,
Beckstrom-Sternberg,S.M., Green,E.D., Powell,J.I., Yang,L.M., Rob., P.G., Hotchkiss,R.N. and Francomano,C.A.,
P.G., Hotchkiss,R.N. and Francomano,C.A.,
SGAP: The Skeletal Genome Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI751993 328 bp mRNA linear EST 20-
cn13a10.x1 Normal Human Trabecular Bone Cells Homo sapiens
clone NHTBC_cn13a10 random, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                    Email: libin@helix.nih.gov
DNA Sequencing and analyses by National
Intramural Sequencing Center (NISC).
Plate: 13 row: a column: 10
Seq primer: -21M13 forward primer (ABI).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 301-402-4877
Fax: 301-496-7157
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Libin Jia
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                                                                                                                                      51
                                                                                                                                      Q
                                                                                                                                 /clone_lib="Normal Human Trabecular Bone Cells"
/note="Organ: Hip; Vector: pBluescript; Site_1:
Library constructed by Dr. Marian Young and Dr.
Gehron Robey (NIDCR)"
119 c 108 g 50 t
                                                                                                                                                                                                                     /tissue_type="Bone"
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/lab_host="SURE"
                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                      /clone="NHTBC_cn13a10"
/sex="Female"
9.13e-14
245.50
75.29%
65.88%
42.04%
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of Health

USA

EcoRI; Pamela

Yang, L.M., Robey

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COMMENT
Percent Similarity:
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Query Match:
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1 (bases 1 to 366)
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                                                                                                                                                                                                                                                                                                                                             Contact: Sanjay Kumar
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOA12-1-E3 HOA
                                                                                                                                                                                                                                                      Email: sanjay_kumar-1@gsk.com
Seq primer: T7.
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: 610-270-7245
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                                                                                                                   /tissue_type="cartilage"
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/clone libe="HOA (Human Osteoarthritic Cartilage)"
/note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
Directional"
                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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 1.04e-13
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Mismatches:
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                                                  Alignment :
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                                                                                                                                                                                                                                          Seq primer:
                                                                                                                                                                                                                                                               Email: sanjay
                                                                                                                                                                                                                                                                                                                                UW2109
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 370)
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HOA33-1-F1 HOA
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 610-270-7245
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709 Swedeland Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Sanjay Kumar
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Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,
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                                                                                                                                                    /organism="Homo sapiens"
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/db xref="taxon:9606"
/tissue_type="cartilage"
/lab host="E.coli DH10 B"
/clome_lib="HOA (Human Osteoarthritic Cartilage)"
/note="Vector: pSPORT I; Site_1: Not
Directional"
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1.05e-13
245.50
74.39%
67.07%
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                Length:
Matches:
Conservative:
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BG898406.1 GI:14308655
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Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
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                                                                                                                                                                                                                                                                                                     Email: sanjay_kumar-1@gsk.com
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                                                                                                                                                                                                                                                                                                                                 Swedeland Road, : 610-270-7245
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                                                                                                                                   /organism="Homo sapiens"

/mol Lype="maNA"

/db_xref="rtaxon:9606"

/tissue type="cartilage"

/lab_host="E.coli_DH10_B"

/clone_lib="HOA (Human Osteoarthritic Cartilage)"

/note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
Directional"
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1.05e-13
245.50
75.29%
65.88%
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Conservative:
Mismatches:
Indels:
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Sathe, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M.
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1. (bases 1 to 372)
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HOA32-1-A8 HOA
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primer: T7.
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/db_xref="ftaxon:906"

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/lab_host="E.coli_DH10_B"

/clone_lib="HOA (Human Osteoarthritic Cartilage)"

/note="Vector: pSPORT I; Site_1: Sall; Site_2: Not
Directional"
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                                                                                                                                                                                                                                                                                                                                                          Email: sanjay_kumar-1@gsk.com
Seq primer: T7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                GlaxoSmithKline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Sanjay Kumar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J. Sathe, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CysCysSerAspLeuGlyProGlnMetLeuArgGluLeuGlnGluThrAsnAlaAlaLeu
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: 610-270-7245
                                                                                                                                                                                                                                                                                                                                                    primer:
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1.06e-13
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67.07%
42.04%
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cn20g10.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA
clone NHTBC_cn20g10 random, mRNA sequence.
AW068338
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Jia, L.B., Young, M.F., Touchman, J.W., Bouffard, G. Beckstrom-Sternberg, S.M., Green, E.D., Powell, J.I., P.G., Hotchkiss, R.N. and Francomano, C.A.
SGAP: The Skeletal Genome Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 LeuLeuAlaLeuAlaAlaValCysSerAlaAlaLysLysGlySerSerLeuGlyGlyAsp
                                                                                                                                                                                                                                                                                                                                                                  Email: libin@helix.nih.gov
DNA Sequencing and analyses by National Institutes of Health
Intramural Sequencing Center (NISC).
Plate: 20 row: g column: 10
Seq primer: M13RP1 reverse primer (ABI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 301-402-4877
Fax: 301-496-7157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    National Human Genome Research Institute 10/10C101, 9000 Rockville Pike, Bethesda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Libin Jia
Medical Genetics Branch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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Library constructed by Dr. Marian Young and Dr.
Gehron Robey (NIDCR)"
a 138 c 124 g 57 t
                                                                                                                                                                                /tissue_type="Bone"
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/lab_host="SURE"
                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1.06e-13
245.50
Length:
Matches:
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20892-1267, USA

Yang, L.M.,

Euteleostomi;

Homo

EST 20-JUN-2002

ProGlnPro

244 47 190 27

364 80 304

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EcoRI; Pamela

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Search completed: August 26, 2003, 19:21:12 Job time: 2942.11 secs
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                                                                                                                                                                                                                                                  Percent Similarity: 74.12%
Best Local Similarity: 65.88%
Ouery Match: 42.04%
DB: 9
                                                                                                              219 GTGATGGAGTGTGACGCGTGCGGGATGCAGCAGTCAGT-ATGCACCGGCCTACCCAGCGT 277
                                      278 GCGGCCCCTGCTCCA 292
                                                                                      68 ValMetGluCysAspAlaCysGlyProGlnProGlnProLysProGlnProGlnProGln 87
                                                                                                                                                                                         ProGlnProLysPro 92
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Mismatches: 18
Indels: 5
Gaps: 1
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Copyright

GenCore version 5.1.6 (c) 1993 - 2003 Compuç

Compugen Ltd

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Result
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Maximum DB
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ster than or equal to the score of the result being printed,
rived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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Listing first 45 summaries
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21 AAY449	AAR14			AAE143	AAY449	22 ABG04441		22 AAU27733	23 AAU80744	AAEJ							23 AAE25032							22 AAM79715			AAM93	ABB82		ABR47	ABJ 05	21 AAB00044	21 AAB00041	AAB000	AAY449
51	60	60	07	96	50	41	31	33	44	05	60	47	48	62	88	36 .	32	49	78	36	22	29	50	15	46	47	97	286	05	20	594	44	41	40	64
Xenopus	PRP 378.	_	Sugarcane	Sugarcane		Novel hu		Human fu	Linker p	Sugarcane	Plasmodium	Human TSP4	Xenopus	Human pro		Target p	Human th	Human th		Camel Ig	nce	Camel 2-	Sequence of	Human pr	Rat cartilage	Human ca		2	Lung can	Breast C	Breast C	Human cart		3	KDEL recep
Xenopus thrombospo	Triticum	æ	e proline	e proline	thrombospond	human diagno	protein SEQ	full-length		d		P4 pentame	ront	protein SEQ		peptide #6	hrombospond	thrombospond	protein SEQ	2-hea	of a	chain Ig h	of hinge	otein SEQ	ilage olig	cartilage ol	polypeptide,	thrombospond	cancer-associ	cancer asso	cancer-asso	rtilage ol	TSP-2	MP/TSP-1 c	eptor inhi

ALIGNMENTS

AAY44963 standard; Protein; 109

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RESULT 1
AAY44963
ID AAY44963
AC AAY4
XX AAYA
AC AAYA
XX XDEI
XX XDEI
XX XDEI
XX XDEI
XX XDEI
XX XDEI
XX Chin
CS CHIN

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                                           10-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric -
Chimeric -
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                                                                                                                    WO200006729-A1.
                                                                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                                                                                Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - Adenovirus E3.
- Homo sapiens.
- Camelus sp.
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                                                                                                                                                                                                                                              /note=
76..99
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                  /label= Signal peptide
/note= "Derived from adenovirus E3'
                                                                                                                                                                                                           "Camel
                                                                                                                                                                                                                                                                                     "Human COMP pentamerisation domain"
                                                                                                                                                                                                  IgG linker domain"
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428.5 422 414.5 371.5 345.5 337.5

receptor receptor receptor

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RESULT 2
AAY44966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                Chimeric
Chimeric
                                                                                          Chimeric - Adenovirus E3
                                                                                                                                      KDEL receptor inhibitor; heat shock protein; immune responigomerisation domain; neoplasia; sarcoma; lymphoma; leu melanoma; carcinoma; glioblastoma; astromytoma; oncogene;
                                                                                                                                                                                              KDEL receptor inhibitor protein-9.
                                                                                                                                                                                                                                23-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The patent discloses the use of KDEL receptor inhibitor to promote secretion of proteins that are normally retained within the cell s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inhibitors of the KDEL receptor which domain useful for promoting secretion retained within the cell -
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                  Peptide
                                                                                                                                                                                                                                                              AAY44966;
                                                                                                                                                                                                                                                                                         AAY44966 standard; Protein; 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 6; 87pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rothman
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                                                                                                                         intections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109;
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                                                                                                                                                                                                                                                                                                                                                                                        ITFLKNTVMECDACGPQPQPKPQPQPQPQPKPQPKPEPEGTGSSEKDEL 109
                                                                                                                                                                                                                                                                                                                                                                                                                            MRYMILGILALAAVCSAAKKGSSIGGDCCSDIGPQMIREIQETNAALQDVRDWIRQQVRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MRYMILGLLALAAVCSAAKKGSSLGGDCCSDLGPQMLRELQETNAALQDVRDWLRQQVRE 60
                                                            Homo sapien
Camelus sp.
                                                                                                                        disease; allergy; autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bonds.
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                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ĀĀ;
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                                                                              sapiens.
/label= Signal_peptide
                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ٥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 584; DB 21;
Pred. No. 7.1e-52;
; Mismatches 0;
                                                                                                                                                                                                                                                                                         ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comprises an oligomerization of proteins which are normal
                                                                                                                                                                immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                    leukaemia;
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RESULT 3
AAY44965
ID AAY4
XX
AC AAY4
XX
DT 23-M
XX
DE KDEL
XX
KW KDEL
KW Olig
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                                                                                                                                                                                                                                                                                                                                                                                                                                          The patent discloses the use of KDEL receptor inhibitor to promote GC secretion of proteins that are normally retained within the cell such as C heat shock proteins by inhibiting KDEL receptor-mediated return of protein complexes to endoplasmic reticulum. This makes the secreted heat shock proteins more accessible to the immune system and improves immune response to a target antigen. The inhibitor protein comprises several subunits where each subunit comprises an oligomerisation domain and has at its carboxy terminus a region which binds to a KDEL receptor. The target antigen may be associated with diseases including neoplasia such as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and as taromytoma, with defective tumour suppressor genes, oncogenes, clifectious diseases, allergy or autoimmune diseases. The present equence is KDEL receptor inhibitor comprising regions encoding a cleavable signal peptide; the oligomerisation domain of human cleavable signal peptide; the oligomerisation domain of human clearation of rat cartilage oligomeric matrix protein which provides increased stability via disulphide bonds.
                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
KDEL receptor inhibitor; heat shock protein; immune response; oligomerisation domain; neoplasia; sarcoma; lymphoma; leukaem
                                                  KDEL receptor inhibitor protein-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 9; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inhibitors of the KDEL receptor which comprises an oligomerization domain useful for promoting secretion of proteins which are normally retained within the cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JUL-1999;
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                                                                                   23-MAY-2000
                                                                                                                                                     AAY44965 standard; Protein; 109 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JUL-1998;
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                                                                                                                                                                                                                                                                   ITFLKNTVMECDACGPQPQPKPQPQPQPQPKPQPKPEPEGTGSSEKDEL 109
                                                                                                                                                                                                                                                                                                                                     MRYMILGLLALAAVCSAAKKGSSLGGDCCSDLGPQMLRELQETNAALQDVRDWLRQQVRE
                                                                                                                                                                                                                                                                                                      MRYMILGLIALAAVCSAAKKGSSLGGDCCGDFNRQFLGQMTQLNQLLGEVKDLLRQQVKE
                                                                                                                                                                                                                                                                                                                                                                                                                                        109 AA;
                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                   (first entry)
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76..99
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30..75
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78.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Derived from adenovirus
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                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                       Score 464; DB 21;
Pred. No. 1.2e-39;
                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                       Length 109;
                                                                                                                                                                                                                                                                                                                                                                        Indels
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60

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RESULT 4
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 shock proteins more accessible to the immune system and improves immune response to a target antigen. The inhibitor protein comprises several subunits where each subunit comprises an oligomerisation domain and has at its carboxy terminus a region which binds to a KDEL receptor. The target antigen may be associated with diseases including neoplasia such
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The patent discloses the use of KDEL receptor inhibitor to promote secretion of proteins that are mormally retained within the cell such as heat shock proteins by inhibiting KDEL receptor-mediated return of protein complexes to endoplasmic reticulum. This makes the secreted heat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 8; 87pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-195296/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SLOK ) SLOAN KETTERING INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                               13
                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                         MSLIRNTIMECQVCGPQPQPKPQPQPQPQPKPQPKPEPEGTGSSEKDEL 109
                                                                                                                                                             ITFLKNTVMECDACGPQPQPKPQPQPQPQPKPQPKPEPEGTGSSEKDEL 109
                                                                                                                                                                                                                  MRYMILGLLALAAVCSAAKKGSSLGGDCCGEQTKALVTQLTLFNQILVELRDDIRDQVKE
                                                                                                                                                                                                                                                        MRYMILGILALAAVCSAAKKGSSIGGDCCSDIGPQMLRELQETNAALQDVRDWLRQQVRE
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                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                              74.3%;
72.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     signal_peptide
"Derived from adenovirus
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Pred. No. 1.4e-36;
3; Mismatches 17;
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The patent discloses the use of KDEL receptor inhibitor to promote secretion of proteins that are normally retained within the cell such as heat shock proteins by inhibiting KDEL receptor-mediated return of protein complexes to endoplasmic reticulum. This makes the secreted heat shock proteins more accessible to the immune system and improves immune response to a target antigen. The inhibitor protein comprises several subunits where each subunit comprises an oligomerisation domain and has at its carboxy terminus a region which binds to a KDEL receptor. The target antigen may be associated with diseases including neoplasia such as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and astromytoma, with defective tumour suppressor genes, oncogenes, infectious diseases, allergy or autoimmune diseases. The present sequence is KDEL receptor inhibitor protein comprising regions including a cleavable signal peptide; the oligomerisation domain from rat cartilage oligomeric matrix protein (COMP); a camel IGG linker domain and the carboxy-terminal sequence KDEL. The subsequence GDCC is an alteration of rat COMP which provides increased stability via disulphide
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The patent discloses the use of KDEL receptor inhibitor to promote secretion of proteins that are normally retained within the cell such as heat shock proteins by inhibiting KDEL receptor-mediated return of protein complexes to endoplasmic reticulum. This makes the secreted heat shock proteins more accessible to the immune system and improves immune response to a target antigen. The inhibitor protein comprises several subunits where each subunit comprises an oligomerisation domain and has at its carboxy terminus a region which binds to a KDEL receptor. The target antigen may be associated with diseases including neoplasia such
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Inhibitors of the KDEL receptor which comprises an oligomerization domain useful for promoting secretion of proteins which are normally retained within the cell -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                 WO200006729-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KDEL receptor inhibitor; heat shock protein; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY44958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                     (SLOK )
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                                                                                            2000-195296/17.
)B; AAZ50492.
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                                                                                                                                                                     ĴΕ,
                                                                                                                                                                                                                     SLOAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----PQPQPKPQPQPQPQPKPQPKPEPEGTGSSEKDEL 109
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Camelus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 AA;
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/note= "Derived from m
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Rat COMP pentamerisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Subsequence from rat COMP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Camel IgG linker domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 422; DB Pred. No. 2.9e 2; Mismatches
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No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mouse Bip"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 21;
.9e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
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Disclosure; Fig

1; 87pp; English.

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RESULT 7
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Chimeric -
Chimeric -
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                                                                                                                                                                                                                                                                                                                                                KDEL receptor inhibitor; heat shock protein; immune response; oligomerisation domain; neoplasia; sarcoma; lymphoma; leukaem melanoma; carcinoma; glioblastoma; astromytoma; oncogene; infectious disease; allergy; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The patent discloses the use of KDEL receptor inhibitor to promote secretion of proteins that are normally retained within the cell such as heat shock proteins by inhibiting KDEL receptor-mediated return of protein complexes to endoplasmic reticulum. This makes the secreted heat shock proteins more accessible to the immune system and improves immune response to a target antigen. The inhibitor protein comprises several
                                                                                                                               Domain
                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                   Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY44962 standard; Protein; 109 AA.
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29-JUL-1998;
                           28-JUL-1999;
                                                        10-FEB-2000.
                                                                                     WO200006729-A1
                                                                                                                                                            Domain
                                                                                                                                                                                                                                  Peptide
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                                                                                                                                                                                                                                                                                           Xenopus sp. Camelus sp.
                                                                                                                                                                                                                                                                             Rattus sp
                                                                                                                                                                                                                                                                                                                         Mus sp.
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98US-0124671
                           99WO-US17147.
                                                                                                                                                                                       /note=
26..30
                                                                                                                               /note=
76..99
                                                                                                                                                                         /note=
                                                                                                                                                                                                                      /label=
                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                            "Xenopus thrombospondin 4 trimerisation
                                                                                                                                                                        "Altered subsequence from rat COMP"
                                                                                                                                                                                                     "Derived from m
                                                                                                              "Camel IgG linker domain'
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                  .eukaemia;
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RESULT 8
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               subunits where each subunit comprises an oligomerisation domain and has at its carboxy terminus a region which binds to a KDEL receptor. The target antigen may be associated with diseases including neoplasia such as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and astromytoma, with defective tumour suppressor genes, oncogenes, infectious diseases, allergy or autoimmune diseases. The present sequence is KDEL receptor inhibitor comprising regions encoding a cleavable signal peptide; the oligomerisation domain of Xenopus thrombospondin 4 (TSP4) trimerisation domain including an additional subsequence; a camel IgG linker domain and the carboxy-terminal sequence KDEL. The subsequence GDCC is an alteration of rat cartilage oligomeric matrix protein which provides increased stability via disulphide bonds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The patent discloses the use of KDEL receptor inhibitor to promote secretion of proteins that are normally retained within the cell such as heat shock proteins by inhibiting KDEL receptor-mediated return of protein complexes to endoplasmic reticulum. This makes the secreted heat shock proteins more accessible to the immune system and improves immune response to a target antigen. The inhibitor protein comprises several
                                                                                                                                                                                               oligomerisation domain; neoplasia; sarcoma; lymphoma; leu melanoma; carcinoma; glioblastoma; astromytoma; oncogene;
                                                                                                                                                                                                                                KDEL receptor inhibitor; heat shock protein; immune response;
                                                                                                                                                                                                                                                               KDEL receptor inhibitor protein-4.
                                                                                                                                                                                                                                                                                                   23-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inhibitors of the KDEL receptor which comprises an oligomerization domain useful for promoting secretion of proteins which are normally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rothman JE,
                                                                                                                 Chimeric
                                                                                                                               Chimeric
                                                                                                                                                  Chimeric -
                                                                 Peptide
                                                                                                                                                                                   intections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 VMECDACGPQPQPKPQPQPQPQPKPQPKPEFEGTGSSEKDEL
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                                                                                                                              Mus sp.
Camelus sp.
                                                                                                                                                                                disease;
                                                                                                                 Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 AA;
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                                                                               Location/Qualifiers
                                /label= Signal_peptide
/note= "Derived from m
/note= "Altered subsequence from rat COMP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ξ,
                                                                                                                                                                                allergy; autoimmune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 371.5; DB 2
Pred. No. 3.2e-30;
3; Mismatches 18
                                from mouse Bip"
                                                                                                                                                                                   disease.
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RESULT 9
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KDEL receptor inhibitor; heat shock protein; immune response; oligomerisation domain; neoplasia; sarcoma; lymphoma; leukaem melanoma; carcinoma; glioblastoma; astromytoma; oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JUL-1999;
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                                                                                                                      receptor inhibitor protein-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLALAAVCSAAKKGSSLGGDCCSDLGPQMLRELQETNAALQDVRDWLRQQVREITFLKNT 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 AA;
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76..99
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Pred. No. 1.4e
14; Mismatches
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Shock proteins more accessible to the immune system and improves immune cresponse to a target antigen. The inhibitor protein comprises several subunits where each subunit comprises an oligomerisation domain and has at its carboxy terminus a region which binds to a KDEL receptor. The target antigen may be associated with diseases including neoplasia such as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and astromytoma, with defective tumour suppressor genes, oncogenes, infectious diseases, allergy or autoimmune diseases. The present sequence is KDEL receptor inhibitor comprising regions encoding a cleavable signal peptide; the oligomerisation domain of mouse thrombospondin 3 (TSP3) trimerisation domain; a camel IgG linker domain and the carboxy-terminal sequence KDEL. The subsequence GDCC is an alteration of rat cartilage oligomeric matrix protein which provides increased stability via disulphide bonds.
                                                                                                                                                                                                               Query Match
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Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The patent discloses the use of KDEL receptor inhibitor to promote secretion of proteins that are normally retained within the cell such as heat shock proteins by inhibiting KDEL receptor-mediated return of protein complexes to endoplasmic reticulum. This makes the secreted heat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inhibitors of the KDEL receptor which comprises an oligomerization domain useful for promoting secretion of proteins which are normal retained within the cell
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N-PSDB; AAZ50494.
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                                          VMECDACGEOPOPOPOPOPOPOPOPOPOPOPOPOPO 109
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30..71
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26..30
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/note= "Derived from mouse Bip"
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Pred. No. 9e-27; 
2; Mismatches 1
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57..80
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30..56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gg.
                              59.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Camel IgG linker domain"
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                              Score 309.5; DB 2: Pred. No. 5.3e-24;
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   Mismatches
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Gaps
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MRYMILGLIALAAVCSAAKKGSSLGGDCCSDLGPQMLRELQETNAALQDVRDWLRQQVRE 60

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8 LLALAAVCSAAKKGSSLGGDCCSDLGPQMLRBLQETNAALQDVRDWLRQQVRBITFLKNT

Query Match Best Local Matches

44.9%;

<u>ن</u>

Score 262.5; DB Pred. No. le-18; 5; Mismatches

9 21;

Indels Length

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Gaps

67

57; Similarity Sequence

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RESULT 11
AAB00040
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                                         the second and third type 1 repeats of human TSP (thrombospondin)-1,

but not the TGF (transforming growth factor)-beta activation region

of human TSP-1. The nucleic acid of TSP (thrombospondin)-1 containing

the second and third type-1 repeats and the COMP (cartilage

oligomeric matrix protein) assembly sequence (COMP/TSP-1) was

produced by PCR (polymerase chain reaction). Expression of COMP/TSP-1

caused inhibition of the growth of tumours in mice models.

Thus the nucleic acids and proteins may be useful for treating

angiogenesis related diseases such as cancer (by reducing the rate of

growth and size of tumours), arthritis, psoriasis, diabetic

retinopathy, corneal graft rejection, and glaucoma. They may also be

used for treating human immunodeficiency virus (HIV) infection.

Anti-angiogenic therapy has little toxicity, does not require the

therapeutic agent to enter tumour cells or cross the blood-brain

barrier, controls tumour growth independently of growth of

tumour cell heterogeneity, and does not induce drug resistance.
                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding chimeric proteins such as cartilage oligomeric matrix protein (COMP)/thrombospondins (TSP)-1 and 2, useful for inhibiting angiogenesis and treating diseases such as cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-514823/46
N-PSDB; AAA47734.
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                                                                                                                                                                                                                                                                                                                                                           Claim 33; Fig 4a-b; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lawler JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-2000; 2000WO-US02482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arthritis; psoriasis; diabetic retinopathy; corneal graft rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human COMP/TSP-1 chimeric protein.
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                                 tumour cell heterogeneity,
                                                                                                                                                                                                                                                                                                                        New nucleic acids are described which encode
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                                 and does not induce drug resistance
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                                                                                                                                                                                                                                                                                                   a protein comprising TSP (thrombospondin)-1,
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                                                                                                                                                                                                                                                                                                     New nucleic acids are described which encode a protein comprising the second and third type I repeats of human TSP (thrombospondin)-1, but not the TGP (transforming growth factor)-beta activation region of but not the TGP (transforming growth factor)-beta activation region of human TSP-1. The nucleic acid of TSP (thrombospondin)-1 containing the second and third type-1 repeats and the COMP (cartilage coligomeric matrix protein) assembly sequence (COMP/TSP-1) was produced by PCR (polymerase chain reaction). Expression of COMP/TSP-1 caused inhibition of the growth of tumours in mice models. Thus the nucleic acids and proteins may be useful for treating can angiogenesis related diseases such as cancer (by reducing the rate of growth and size of tumours), arthritis, psoriasis, diabetic retinopathy, corneal graft rejection, and glaucoma. They may also be used for treating human immunodeficiency virus (HIV) infection. Anti-angiogenic therapy has little toxicity, does not require the therapeutic agent to enter tumour cells or cross the blood-brain controls tumour growth independently of growth of tumour cell heterogeneity, and does not induce drug resistance.
                                                                                                                                                             Query Match
Best Local :
                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding chimeric proteins such as cartilage oligomeric matrix protein (COMP)/thrombospondins (TSP)-1 and 2, useful for inhibiting anglogenesis and treating diseases such as cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 50; Fig 5a-b; 40pp;
                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSP-1; TSP-2; COMP; cartilage oligomeric matrix protein; thrombospondin; angiogenesis; tumour; treatment; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human COMP/TSP-2 chimeric protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000-514823/46.
DB; AAA47735.
            10
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                                                                                                                                                             Similarity
   LLTLAALGASGQGQSPLG----SDLGPQMLRELQETNAALQDVRDWLRQQVREITFLKNT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VMECDACGMQQSVRTGLPSVRP 87
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                                                                                                                                                                                                                                                       300
                                                                                                                                Conservative
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••
                                                                                                                       Score 262.5; DB 21;
Pred. No. 1.4e-18;
5; Mismatches 9;
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                                                                                                                                                                                       DB 21;
                                                                                                                             Indels
                                                                                                                                                                                       Length 300;
                                                                                                                             11;
                                                                                                                             Gaps
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RESULT 13
AAB00044
                            New nucleic acids are described which encode a protein comprising CC the second and third type I repeats of human TSP (thrombospondin)-1, CC but not the TGF (transforming growth factor)-beta activation region CC of human TSP-1. The nucleic acid of TSP (thrombospondin)-1 containing the second and third type-1 repeats and the COMP (cartilage colloqueric matrix protein) assembly sequence (COMP/TSP-1) was protein assembly sequence (COMP/TSP-1) was protein assembly sequence (COMP/TSP-1) caused inhibition of the growth of tumours in mice models. Thus the nucleic acids and proteins may be useful for treating CC angiogenesis related diseases such as cancer (by reducing the rate of cartinopathy, corneal graft rejection, and glaucoma. They may also be used for treating human immunodeficiency virus (HIV) infection. CC used for treating human immunodeficiency virus the blood-brain controls tumour growth independently of growth of the protein growth of the protein growth independently of growth of the protein controls tumour growth independently of growth of the protein controls tumour growth independently of growth of the protein controls tumour growth independently of growth of the protein controls the protein growth independently of growth of the protein controls the protein growth independently of growth of the protein controls the protein growth independently of growth of the protein controls the protein growth independently of growth of growth of the protein growth independently of growth of growth of the protein growth growth of growth 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 3; 40pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arthritis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT
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cell heterogeneity,
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RESULT 14
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                        The invention comprises a method of detecting a breast cancer-associated CC transcript in a cell from a patient. The method of the invention involves CC contacting a biological sample from the patient with a nucleotide that CC hybridises to one of the 69 breast cancer-associated gene sequences shown in the specification. The method of the invention is useful in the CC diagnosis or prognosis of breast cancer, and for detecting genes that are CC up or down-regulated in breast cancer cells. Genes identified by the CC method of the invention can be used in diagnostic purposes and also as CC targets for screening for therapeutic compounds that modulate breast CC cancer (e.g. hormones or antibodies). Identification of genes that are CC over or under expressed in breast cancer can additionally provide high-cc resolution, high-sensitivity datasets which can be used in the areas of CC diagnostics, therapeutics, drug development, pharmacogenetics, protein CC structure and blosensor development. Amino acid sequences ABJ05536 - CC ABJ05604 represent the proteins encoded by the 69 breast cancer-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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02-FEB-2001; 2001US-265928P.
09-APR-2001; 2001US-282698P.
09-APR-2001; 2001US-0829472.
04-MAY-2001; 2001US-288590P.
29-MAY-2001; 2001US-294443P.
                                                                                                                                                                                                                                                                                                                         Detecting a breast cancer-associated transcript in a patient's cell, useful for diagnosing breast cancer, comprises contacting a biological sample with a polynucleotide that selectively hybridizes with breast cancer nucleic acids
                                                                                                                                                                                                                                                                                            Disclosure; Page 401; 414pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mack DH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BIOTECHNOLOGY INC.
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nt; pharmacogenetics; biosensor developm
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Sequence

757

Sequence

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27-JUN-2001; 2001US-301572P.
18-JUL-2001; 2001US-3056501P.
25-SEP-2001; 2001US-325002P.
05-MAR-2002; 2002US-362585P.
14-MAY-2002; 2002US-380391P.
                                                                   The present invention describes a method for assessing whether a patient is afflicted with breast cancer. The method comprises comparing the level of expression of a marker (gene/polypeptide see ACC50076 to ACC5034 and ABR47386 to ABR47632) in a patient sample and the normal level of expression of the marker in a control non-breast cancer sample, where a significant increase in the level of expression of the marker in the patient is afflicted with breast cancer. The breast cancer associated sequences from the present invention have cytostatic activities and can be used in gene therapy. The method is useful for diagnosing and treating breast
                                                                                                                                                                                                                                        Breast cancer diagnosis or treatment expression of a marker in a patient sonon-breast cancer sample -
                                                                                                                                                                                                                                                                                                         WPI;
                                   N.B. The seque specification,
                                                                                                                                                                                                                 Claim 1; SEQ ID 72; 128pp; English.
                                                                                                                                                                                                                                                                                            N-PSDB;
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                                                              cancer
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                                   The sequence data for this patent did not ification, but was obtained in electronic i
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, Myer V, Wang Y, Xu Y,
GN, Pusztai L, Meric F,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002WO-US19669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer; cytostatic; gene therapy
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Zhao X,
Sahin A,
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Result
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Maximum DB
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Maximum Match 100%
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Match
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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                   US-09-124-671-23
US-09-124-671-29
US-09-124-671-15
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US-09-124-671-2
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US-08-466-7302-38
US-08-467-282B-38
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US-08-467-282B-34
US-08-467-282B-44
US-08-468-7392-44
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US-08-468-7392-44
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US-08-468-7392-44
US-08-468-7392-44
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Sequence 29,
Sequence 27,
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o. 6160088
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16.8	17.0	17.3	17.5	18.3	18.5	18.7	19.0	19.3	19.9	20.0	20.4	20.7	23.7	24.7	24.9	25.0	25.0
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US-08-465-746-2	US-09-328-352-7276	US-09-252-991A-19088	US-08-714-741-32	US-09-345-473E-39	US-09-252-991A-23116	US-09-252-991A-17202	US-09-069-023-22	US-08-989-299-12	US-09-602-565-34	US-09-124-671-6	US-08-718-661-2	US-09-124-671-5	PCT-US93-11725-2	US-09-379-297-5	PCT-US93-11725-4	US-08-468-739C-87	US-08-466-710C-87
Sequence 2, Appli	Sequence 7276, Ap	Sequence 19088, A	Sequence 32, Appl	Sequence 39, Appl	Sequence 23116, A	Sequence 17202, A	Sequence 22, Appl	Sequence 12, Appl		Sequence 6, Appli	Sequence 2, Appli	Seguence 5, Appli	Sequence 2, Appli	Sequence 5, Appli	Sequence 4, Appli	Sequence 87, Appl	Sequence 87, Appl

ALIGNMENTS

Application US/09124671A

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GENERAL INFORMATION:
APPLICANT: ROCHMAN, James
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hoé, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 23
LENGTH: 109
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
COMMENT NUCLEARIES
                                                                                                                                                                                                                                                                                          RESULT 2
US-09-124-671-29
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                                                                                                                                                                                                                                               Sequence 29, Application US/09124671A Patent No. 6160088
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Best Local Similarity
Matches 109; Conserv
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APPLICANT: Mayhew, Mark
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Pred. No. 2.2e-57;
; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: Rothman, James
APPLICANT: Mayhew, Mark
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 15
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APPLICANT: Nothman, James
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31468
CURRENT APPLICATION UNMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 27
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Sequence 27, App...
No. 6160088
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ORGANISM: Artificial Sequence
FEATURE:
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TYPE: PRT
TYPE: ORGANISM: Artificial Sequence
FEATURE:
TYPE: PRT ORGANISM: Artificial Sequence
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                                         ENGTH: 115
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85; Conserv
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79; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74.3%; Score 434; DB 3; Length 109; 72.5%; Pred. No. 8.7e-41; tive 13; Mismatches 17; Indels
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APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 34
FENCION:
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; OTHER INFORMATION: chimeric rat COMP-KDEL
US-09-124-671-15
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; OTHER INFORMATION: chimeric rat comp
US-09-124-671-13
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                                                                                                                                                                                                          Sequence 13, Application US/09124671A
Patent No. 6160088
GENERAL INFORMATION:
APPLICANT: ROthman, James
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
                                                                                                    FILE REFERENCE: 31488
CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 13
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Best Local Similarity 77.7
Matches 87; Conservative
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Best Local Similarity 82.8%;
Matches 82; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Rothman, James APPLICANT: Mayhew, Mark APPLICANT: Hoe, Mee
                                  TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 134
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                      LENGTH: 115
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77.7%;
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Pred. No. 3.8e-40;
3; Mismatches 5
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Pred. No. 2.4e-39;
2; Mismatches 1
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RESULT 8
US-09-124-671-19
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                                                     US-09-124-671-19
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                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21, 555
Sequence 21, 555
No. 6160088
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                      Query Match
                                                                                                                                                                                                                                                                                                                                                             Patent No.
 Best Local Similarity
                                                                                                                                                                                                                                                 APPLICANT: Rothman, James
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Rothman, James
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 31488
CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 109
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                     LENGTH: 109
TYPE: PRT
ORGANIEM: Artificial Sequence
FEATURE:
FEATURE:
                                                                      OTHER INFORMATION: chimeric mouse TSP3-KDEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: chimeric Kenopus laevis TSP4-KDEL
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76.8%;
 59.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.6%; Score 371.5; DB 3
66.7%; Pred. No. 7.2e-34;
tive 13; Mismatches 18
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Pred. No. 1.3e-38;
3; Mismatches 6
Score 345.5; DB 3; Pred. No. 5.4e-31;
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                  Length 109;
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                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Rothman, James
APPLICANT: Mayhew, Mark
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Patent No. 6160088
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Patent No. 6160088
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CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
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TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
FILE REFERENCE: "NUMBER 115/09/124.671A
                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/124,671A CURRENT FILING DATE: 1998-07-29
                                                                                                                                                                                                                                                                                             FILE REFERENCE: 31488
                                                                                                                                                                                                                                                                                                       APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rothman, James
APPLICANT: Mayhew, Mark
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                                                                                                                       OTHER INFORMATION: chimeric human PLB-KDEL
                                                                                                                                       FEATURE:
                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                       TYPE: PRT
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1 MRYMILGLLALAAVCSAAKKGSSLGGDCCSDLGPQMLRELQETNAALQDVRDWLRQQVRE 60
                                                  Similarity
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    Mismatches

                                                  Score 309.5; DB 3; Pred. No. 4.1e-27;
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Pred. No. 4e-
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GENERAL INFORMATION:
APPLICANT: Rochman, James
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITILE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31486
CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
RESULT 13
US-09-091-814-45
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US-09-124-671-2
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-124-671-2
                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/091,814
CURRENT FILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 46, Application US/09091814
Patent No. 6218513
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Best Local Similarity
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Best Local
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APPLICANT: Epp, Janet K
APPLICANT: Kerwin, Bruce A.
APPLICANT: Olins O., Peter
APPLICANT: Mathews J., Antony
TITLE OF INVENTION: GLOBINS CONTAINING BINDING DOMAINS
FILE REFERENCE: BXTB2005
                                                                                                                                                                                                                                     LENGTH: 66
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Human COMP
OTHER INFORMATION: domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 SDLGPQMLRELQETNAALQDVRDWLRQQVREITFLKNTVMECDACG 75
                                                                                             22 SSLGGDCCSDLGPQMLREL-QETNAALQDVRDWLRQQVREITFLKNTVMECDACGPQ 77
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                                                                       4 SPLG----SDLGPQMLRELQQETNAALQDVRDWLRQQVREITFLKNTVMECDACGMQ 56
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100.0%; Pred. No. 6.8e-20;
                                                                                                                                                                    40.2%;
87.7%;
                                                                                                                                                Score 234.5; DB 3;
Pred. No. 5.6e-19;
0; Mismatches 2;
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RESULT 14
US-09-124-671-1
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; OTHER INFORMATION: domain
US-09-091-814-45
                                                                                                                                                                                                     RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-124-671-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09124671A Patent No. 6160088 GENERAL INFORMATION:
                                                                                                                                               Sequence 38, Application US/08471780C Patent No. 5759808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 45
                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 45, Application US/09091814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
           GENERAL INFORMATION:

APPLICANT: Casterman, Cecile
APPLICANT: Hamers, Raymond
TITLE OF INVENTION: Immunoglobulins
NUMBER OF SEQUENCES: 130

CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Fa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Olins O., Peter
APPLICANT: Mathews J., Antony
TITLE OF INVENTION: GLOSINS CONTAINING BINDING DOMAINS
FILE REFERENCE: BXTB2005
CURRENT APPLICATION NUMBER: US/09/091,814
CURRENT FILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rothman, James APPLICANT: Mayhew, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Anthony-Cahill, APPLICANT: Epp, Janet K
APPLICANT: Kerwin, Bruce A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hoe, Mee
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 46
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Ratus ratus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH:
                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
                                                                                                                                                                                                                                                                               31 DLGPQMLRELQETNAALQDVRDWLRQQVREITFLKNTVMECDACG 75
                                                                                                                                                                                                                                                                                                                                      41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 LGGDCCSDLGPQMLRELQETNAALQDVRDWLRQQVREITFLKNTVMECDACGPQPQPQFKP
                                                                                                                                                                                                                                                              N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGG----DLAPQMLRELQETNAALQDVRELLRQQVKEITFLKNTVMECDACGMQPARTP 60
1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                      36.1%;
ilarity 91.1%;
Conservative
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                                                                                                                                                                                                                                                                                                                                    Score 211; DB 3;
Pred. No. 1.4e-16;
2; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2
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Pred. No. 2.8e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                   Farabow,
                                                                       Devoid of Light Chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                                                                                                                                                        Length 46;
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COUNTRY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 2006-3155

COUNTRY: USA
ZIP: 2006-3155

COUNTRY: 2006-3155

COUNTRY: 2006-3155

COUNTRY: 2006-3155

COMPUTER READABLE FORM:
COMPUTER: IFM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATION NUMBER: PR 92402326.0

PRIOR APPLICATION NUMBER: PR 92402326.0

PRIOR APPLICATION NUMBER: PR 93401310.3

PRILING DATE: 17-AUC-1992
PRIOR APPLICATION NUMBER: PR 93401310.3

PRILING DATE: 21-AUG-1992
PRIOR APPLICATION NUMBER: PR 93401310.3

PRILING DATE: 21-AUG-1992
PRIOR APPLICATION NUMBER: PR 93401310.3

PRILING DATE: 21-AUG-1993
ATTORNEY/AGENT INFORMATION:

REFERENCE/DOCKET NUMBER: 09580.0008-00000

TELEPHONE: 202-408-400

TELEPHONE: 202-408-400

INFORMATION FOR SED ID NO: 38:
CENTER TYPE: anino acids

TYPE: TYPE: Single

TYPE: Anino acids

TYPE: ANINORMATION: /label= hinge

US-ON-471-780C-38

OUCHTY MATCH

TOPOLOGY: linear

NOLECULE TYPE: peptide

PRIOR TYPE: ANINORMATION: /label= hinge

US-ON-471-780C-38

OUCHTY MATCH

TOPOLOGY: linear

NOLECULE TYPE: peptide

PRIOR TYPE: AUG-135: SCOTE 146; DB 1; Length 35;

DENTITY STATEMENT STATEME
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
Published_Applications_AA:*

1: /cgn2_6/ptcdata/1/pubpaa/PCT_NEW_PUB.pep:*

2: /cgn2_6/ptcdata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptcdata/1/pubpaa/USO6_NEW_PUB.pep:*

4: /cgn2_6/ptcdata/1/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptcdata/1/pubpaa/USO8_PUBCOMB.pep:*

6: /cgn2_6/ptcdata/1/pubpaa/USO8_NEW_PUB.pep:*

7: /cgn2_6/ptcdata/1/pubpaa/USO8_PUBCOMB.pep:*

8: /cgn2_6/ptcdata/1/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptcdata/1/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptcdata/1/pubpaa/USO9E_PUBCOMB.pep:*

11: /cgn2_6/ptcdata/1/pubpaa/USO9E_PUBCOMB.pep:*

12: /cgn2_6/ptcdata/1/pubpaa/USO9E_PUBCOMB.pep:*

13: /cgn2_6/ptcdata/1/pubpaa/USO9E_PUBCOMB.pep:*

14: /cgn2_6/ptcdata/1/pubpaa/USO9E_PUBCOMB.pep:*

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17: /cgn2_6/ptcdata/1/pubpaa/USO9_PUBCOMB.pep:*

18: /cgn2_6/ptcdata/1/pubpaa/USO9_PUBCOMB.pep:*

19: /cgn2_6/ptcdata/1/pubpaa/USO9_PUBCOMB.pep:*

19: /cgn2_6/ptcdata/1/pubpaa/USO9_PUBCOMB.pep:*

10: /cgn2_6/ptcdata/1/pubpaa/USO9_PUBCOMB.pep:*

10: /cgn2_6/ptcdata/1/pubpaa/USO9_PUBCOMB.pep:*
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584
1 MRYMILGLLALAAVCSAAKK......PKPQPKPEPEGTGSSEKDEL 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  August 26, 2003, 16:02:18; Search time 38.5841 Seconds (without alignments) 372.792 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    497079 seqs, 131961718 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               497079
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 2 3 3 4 4 4 7 6 8 8 8 9 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
262.5 262.5 262.5 262.5 262.5 145.5 1145.5 1145.5 1145.1 1156 1126 1126 1136 1137.5 1137.5	Score
1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	Query Match
300 300 757 757 757 961 103 503 503 503 503 503 503 503 503 503 5	Query Match Length DB
110	
US-09-919-603-7 US-09-919-603-7 US-09-919-603-3 US-10-301-822-41 US-10-177-293-72 US-10-10-17-293-72 US-10-154-971-24 US-10-156-761-12544 US-10-156-761-12544 US-10-301-822-155 US-10-301-822-155 US-10-301-822-17 US-09-881-758A-228 US-10-182-21-7 US-09-738-626-6457	ID
Sequence 5, Appli Sequence 7, Appli Sequence 3, Appli Sequence 41, Appl Sequence 72, Appl Sequence 22, Appli Sequence 24, Appl Sequence 12544, Appl Sequence 17, Appl Sequence 17, Appl Sequence 28, Appl Sequence 27, Appli Sequence 27, Appli Sequence 967, Appli Sequence 967, Appli	Description

ALIGNMENTS

RESULT 1 US-09-919-603-5

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; OTHER INFORMATION: chimeric protein
US-09-919-603-5
                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/118,053
PRIOR FILING DATE: 1999-02-01
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 242
TYPE: PRI
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Lawler, John W.
TITLE OP INVENTION: COMP/TSP-1, COMP/TSP-2 and Other TSP
TITLE OP INVENTION: Chimeric Proteins
FILE REFERENCE: 1440.1033-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/09919603
Patent No. US20020137679A1
                                                                                                                                                                      Matches
                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/919,603
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: PCT/US00/02482
PRIOR FILING DATE: 2000-02-01
99
                                       68 VMECDACGPQ-----PQPKP 82
                                                                                 10 LLTLAALGASGQGQSPLG----SDLGPQMLRELQETNAALQDVRDWLRQQVREITFLKNT 65
                                                                                                         8 LIALAAVCSAAKKGSSIGGDCCSDLGPQMLRELQETNAALQDVRDWLRQQVREITFLKNT 67
                                                                                                                                                                    57;
VMECDACGMQQSVRTGLPSVRP 87
                                                                                                                                                                    Conservative
                                                                                                                                                             44.9%; Score 262.5; DB 10;
69.5%; Pred. No. 3.6e-18;
c. Mismatches 9;
                                                                                                                                                                                                         DB 10;
                                                                                                                                                                    Indels
                                                                                                                                                                                                         Length 242;
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                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                       LENGTH: 757
TYPE: PRT
ORGANISM: Homo sapiens
US-09-919-603-3
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APPLICANT: Lawler, John W.
TITLE OF INVENTION: COMP/TSP-1, COMP/TSP-2 and
TITLE OF INVENTION: Chimeric Proteins
FILE REFERENCE: 1440.1033-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09919603 Patent No. US20020137679A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/09919603
Patent No. US20020137679A1
                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 44.9%; Score 262.5; DB 1
Best Local Similarity 69.5%; Pred. No. 4.6e-18;
Matches 57; Conservative 5; Mismatches 9
                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lawler, John W.

TITLE OF INVENTION: COMP/TSP-1, COMP/TSP-2 and
TITLE OF INVENTION: Chimeric Proteins
FILE REFERENCE: 1440.1033-007
CURRENT APPLICATION NUMBER: US/09/919,603
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: PCT/US00/02482
PRIOR FILING DATE: 2000-02-01
PRIOR FILING DATE: 2000-02-01
                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/118,053
PRIOR FILING DATE: 1999-02-01
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/919,603
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: PCT/US00/02482
PRIOR FILING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: 60/118,053
PRIOR FILING DATE: 1999-02-01
NUMBER OF SEQ ID NOS: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 300
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                       Local
                                          68 VMECDACGPQ-----PQPKP 82
                                                                                       10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 LLTLAALGASGQGQSPLG----SDLGPQMLRELQETNAALQDVRDWLRQQVREITFLKNT 65
                                                                                                                                                                                 57;
                                                                                                               8 LLALAAVCSAAKKGSSLGGDCCSDLGPQMLRELQETNAALQDVRDWLRQQVREITFLKNT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 LLALAAVCSAAKKGSSLGGDCCSDLGPQMLRELQETNAALQDVRDWLRQQVRBITFLKNT 67
                                                                                                                                                                                                       Similarity
                                                                                     LLTLAALGASGQGQSPLG----SDLGPQMLRELQETNAALQDVRDWLRQQVREITFLKNT 65
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VMECDACGMQQSVRTGLPSVRP 87
                                                                                                                                                                                 Conservative
                                                                                                                                                                                                    44.9%;
                                                                                                                                                                             Score 262.5; DB 10;
Pred. No. 1.3e-17;
5; Mismatches 9;
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                                                                                                                                                                                                                       Length 757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
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; ORGANISM: Homo Sapiens
US-10-301-822-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         문
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 4
US-10-301-822-41
                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Glatt, Karen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 41
LENGTH: 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals,
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 72, Application US/1U1
Publication No. US20030124128A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 41, Application US/10301822
Publication No. US20030148410A1
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Best Local
                                                         APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
FILE REFERENCE: MEMO1-029P2RNM
CURRENT APPLICATION NUMBER: US/10/301,822
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
                                                                                                                    APPLICANT:
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER FILE REFERENCE: MRI-038
                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 VMECDÁCGMQQSVRTGLÞSVRÞ 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 VMECDACGPQ-----PQPKP 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 LLTLAALGASGQGQSPLG----SDLGPQMLRELQETNAALQDVRDWLRQQVREITFLKNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.9%;
1 Similarity 69.5%;
57; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 LLALAAVCSAAKKGSSLGGDCCSDLGPQMLRELQETNAALQDVRDWLRQQVREITFLKNT
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                                                         Meric, Funda
Sahin, Aysegul
Mills, Gordon B.
                                                                                                                    Hortobagyi,
Pusztai, La
                                                                                                                                         Bast Jr., Robert C.
Hortobagyi, Gabriel
                                                                                                                                                                                                                                                            Wang,
                                                                                                                                                                                                                                                                                                        Kamatkar, Shubhai
Mertens, Maureen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/10177293
                                                                                                                                                                               Meyers, Rachel E.
                                                                                                                                                                                                                                                                                                                                            Gannavarpu, Manjula
                                                                                                                                                                                                                                                                                                                                                                      Zhao, Xumei
                                                                                                                                                                                                   Monahan, John
                                                                                                                                                                                                                      Hoersch,
                                                                                                                                                                                                                                           Yongyao
                                                                                                                                                                                                                                                                Youzhen
                                                                                                                                                                                                                                                                                     O<sub>T</sub>C
                                                                                                                    Lajos
                                                                                                                                                                                                                          Sebastian
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Pred. No. 1.3e-17;
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; ORGANISM: Homo sapiens
US-10-017-721-4
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RESULT 7
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/10017721 Publication No. US20030096248A1
                                                                                                                                                                                                                 Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/017,721
CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/317,033
PRIOR FILING DATE: 2001-09-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: McCarthy, Jeanette
APPLICANT: Daley, George
APPLICANT: Bolk, Stacey
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
FILE REFERENCE: MMI-003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/325,002
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/362,585
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/xxx,xxx
PRIOR FILING DATE: 2002-05-14
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PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: US 60/301,572
PRIOR FILING DATE: 2001-06-27
                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/330,248
PRIOR FILING DATE: 2001-10-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/177,293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0
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TYPE: PRT
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                                                      278 AP-PAPPTRP 286
                                                                                           вт ороркроркр 96
                                                                                                                                                                      31 DIGPOMIRELQETNAALQDVRDWIRQQVREITFIKNTVMECDACGP----QPQPKPQPQP
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                                                                                                                                  DFNRQFLGQMTQLNQLLGEVKDLLRQQVKETSFLRNTIAECQACGPLKFQSPTPSTVVAP
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                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                         24.9%; Score 145.5; DB 15;
42.9%; Pred. No. 5.3e-06;
Mismatches 25;
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Pred. No. 1.3e-17;
                                                                                                                                                                                                                                                 DB 15;
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                                                                                                                                                                                                                                                   961;
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; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-10-154-971-22
                                                                                                                                                                                                                                                                                  US-10-154-971-24
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                                                                                                                                                                                                                   Sequence 24, Application US/10154971 Publication No. US20030088074A1 GENERAL INFORMATION:
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Publication No. US20030088074A1
GENERAL INFORMATION:
APPLICANT: Hamers, Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 202-414-400
TELEPAX: 202-414-4040
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENCER & FRANK
-STREET: 1100 New York Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Gollin, Michael A.
REGISTRATION NUMBER: 31,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENCER & FRANK
STREET: 1100 New York Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                     Muyldermans, Serge
TITLE OF INVENTION: VARIABLE FRAGMENTS OF IMMUNOGLOBULING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                    76 POPOPKPOPOPOPOPKPOPKPEPEGTG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
CITY: Washington
STATE: DC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 178 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/EP96/01725
FILING DATE: 25-APR-1996
APPLICATION NUMBER: EP 95400932.0
FILING DATE: 25-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/10/154,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                 Hamers, Raymond
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                                                                                                                                         USE FOR THERAPEUTIC
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Pred. No. 2.7e-06;
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                                                          N.W.,
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Ψ.
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                                                          Suite 300 East
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 178;
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LENGTH: 303 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-154-971-24
                                                                                 PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 12544
LENGTH: 578
LENGTH: 578
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-12544
                                                                                                                                                                                                                                                   APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
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Best Local :
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APPLICANT:
APPLICANT:
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  Matches
                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 202-414-4040 INFORMATION FOR SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/945,244
FILING DATE: CUNKNOWN:
APPLICATION NUMBER: PCT/EP96/01725
FILING DATE: 25-APR-1996
APPLICATION NUMBER: EP 95400932.0
FILING DATE: 25-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: GOllin, Michael A.
REGISTRATION NUMBER: 31,957
REFERRENCE/DOCKET NUMBER: GUPLA 0003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-414-4000
  Local Similarity 79.2
nes 19; Conservative
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PRIOR APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 PQPQPKPQPQPQPQPKPQPKPEP 98
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ISHIKAWA, JUN
HORIKAWA, HIROSHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.8%; Score 139; DB 15; nilarity 100.0%; Pred. No. 6.2e-06; Conservative 0; Mismatches 0;
                 21.6%;
Score 126; DB 15;
Pred. No. 0.00024;
5; Mismatches 0;
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                                       Length 578;
  Indels
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  Gaps
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APPLICANT: Arvizu, Chandra S.
APPLICANT: Corley, Neil C.
APPLICANT: Corley, Neil C.
APPLICANT: Gorley, Neil C.
APPLICANT: Gorley, Neil C.
APPLICANT: Gorley Corley
FIILE OF INVENTION: MOLECULE ASSOCIATED WITH APOPTOSIS
FILE REFERENCE: PC-0018-1 CIP
CURRENT APPLICATION NUMBER: US/10/280,953
CURRENT FILING DATE: 2002-10-23
PRIOR APPLICATION NUMBER: 09/602,565
PRIOR FILING DATE: 2000-06-22
PRIOR FILING DATE: 1998-06-29
PRIOR FILING DATE: 1998-06-29
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; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-301-822-155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
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US-10-280-953-17
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CURRENT APPLICATION NUMBER: US/10/301,822
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/361,988
PRIOR PRICING DATE: 2002-03-05
PRIOR PILING DATE: 2002-05-20
PRIOR FILING DATE: 2002-05-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 155
                                                                                                                                                   NUMBER OF SEQ ID NOS: 17
SOFTWARE: PERL Program
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Yue, Henry
APPLICANT: Arvizu, Cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 79.2 Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Publication No. US20030148410A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF COLON CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Millennium Pharmaceuticals, Inc. APPLICANT: Berger, Allison APPLICANT: Guillemette, Tracy L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030113317A1 g1469400
                                                                                                     LENGTH: 261
TYPE: PRT
                                                                              ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POPOPOPOPOPOPOPOPOPOPOPO
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Schlegel, Robert
Monahan, John E.
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79.2%;
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Pred. No. 0.0004;
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; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 807
; TYPE: PRT
; ORGANISM: Zea mays
US-10-138-221-7
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; ORGANISM: Helicobacter pylori
US-09-881-752A-228
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/10138221 Publication No. US20020199216A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 228
LENGTH: 285
                                                                              Matches
                                                                                              Query Match
Best Local Similarity
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APPLICANT: Tomb, Jean-Francois
APPLICANT: Oomen, Raymond P.
TITLE OF INVENTION: Identification of Polymucleotides
TITLE OF INVENTION: Encoding No. US20020115078A1el Helicobacter Polypeptides
TITLE OF INVENTION: Genome
FILE REFERENCE: 06132/041002
CURRENT APPLICATION NUMBER: US/09/881,752A
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 08/833,457
PRIOR PILING DATE: 1997-04-01
                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: USE OF TRANSPOSABLE ELEMENTS FOR ALTERING GENE EXPRESSION FILE REFERENCE: 51178/7 CURRENT APPLICATION NUMBER: US/10/138,221 CURRENT FILING DATE: 2002-08-01 PRIOR APPLICATION NUMBER: US 60/287,882 PRIOR APPLICATION NUMBER: US 60/287,882 PRIOR FILING DATE: 2001-05-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kleanthous, Harold
APPLICANT: Al-Garawi, Amal
APPLICANT: Miller, Charles
APPLICANT: Tomb, Jean-Francois
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Amy F. MacRae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 370
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108 EPOPOPOPOPEPOPOPOPEPEEE 130
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                    76 PQPQPKPQPQPQPQPKPQPKPEPE 99
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                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                            19.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.7%; Score 115; DB 10; Length 285; 66.7%; Pred. No. 0.0013; tive 8; Mismatches 0; Indels (
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                                                                                        Score 111; DB 14;
Pred. No. 0.011;
                                                                              Mismatches
                                                                                                               Length 807;
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; ORGANISM: Homo sapiens
US-09-764-864-967
                                                                                                                                                                                                                ; ORGANISM: Corynebacterium glutamicum US-09-738-626-6457
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US-09-764-864-967
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                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN ver. 3.0
SEQ ID NO 6457
LENGTH: 266
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Best Local Similarity 70.8%;
Matches 17; Conservative
                                                                                                                                    Matches
                                                                                                                                                      Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231 POPOPOPPPOPEPRSVPOPEPEPE 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 PQPQPKPQPQPQPKPQPKPEPE 99
                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIZOGUCHI,
                                                                                                                                  Conservative
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Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 967
LENGTH: 316
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, WASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
                                                                  138 QLEEMRTQLSELSGREWGYEPTMLRAEARRILELESQQLSQQFQAPQPEVPEPVAVPEPM 197
84 PQPQPQPKPQPKPEPEGTGSSEKDE 108
                                                                                                             39 ELQETNAALQDV--RDW-----LRQQVREITFLKNTVMECDACGPQPQ------PKPQ 83
                                                                                                                                                           18.4%; Score 107.5; DB 10; 29.4%; Pred. No. 0.0067; tive 16; Mismatches 29;
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Pred. No. 0.00
4; Mismatches
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                                                                                                                                                                                                        Length 266;
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ed: 5841	PEPA
Search completed: August 26, 2003, 16:07:06 Job time : 39.5841 secs	198 PEPAPVPEPVPEPEPVEVAVEAEEE 222
26,	PEPE
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2003 Compugen Ltd.
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		•	
RESULT 2 \$33598 Ig gamma-2 chain - Arabian camel (fragment) C;Species: Camelus dromedarius (Arabian camel) C;Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 11-Jan-2000 C;Accession: \$33598 R;Hamers-Casterman, C:; Atarhouch, T.; Muyldermans, S.; Robinson, G.; Hamers, C.; Songa, Nature 363, 446-448, 1993 A;Title: Naturally occurring antibodies devoid of light chains. A;Reference number: \$33598; MUID:93275410; PMID:8502296 A;Accession: \$33598; MUID:93275410; PMID:8502296 A;Accession: \$33598 A;Status: not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-135 <41AM> A;Experimental source: Spleen C;Kevvords: disulfide bond: immunoglobulin homology	Matches 51; Conservative 8; Mismatches 18; Indels 4; Gaps 1; Qy 8 LIALAAVCSAAKKGSSLGGDCCSDLGPQMLRELQETNAALQDVRBWLRQQVREITFLKNT 67	ALIGNMENTS Pe oligomeric matrix protein precursor ate names: thrombospondin homolog COMI sea Rattus norvegicus (Norway rat) 30-Apr-193 #sequence_revision 03-May.ion: A44315 Chem. 267, 22346-22350, 1992 COMP (cartilage oligomeric matrix prosion: A44315 idon: A44315; MUID:93054522; PM. sion: A44315 references: GB:X72914; NID:9297438; PM. ses: 1-755 < OLD> references: GB:X72914; NID:9297438; PM. seguence extracted from NCBI backbone sequence extracted from NCBI backbone sequence extracted from Seguence sequence extracted from Seguence extracted from	30 111 19.0 427 2 T03955 probable transposa 31 111 19.0 807 2 T02916 hypothetical prote 32 111 19.0 1749 2 S75138 hypothetical prote 33 110.5 18.9 149 2 B96651 protein T3P18.7 [i 34 110 18.8 792 2 F90566 35 108.5 18.6 312 2 B84632 protein fupo 36 108 18.5 266 2 T44781 tonB protein [impo 37 107 18.3 437 2 T26767 hypothetical prote 38 107 18.3 633 1 S49611 39 107 18.3 633 1 S49611 conserved hypothet 40 105 18.0 873 2 F90070 probable serine/th 41 104 17.8 949 2 T98658 42 104 17.8 1569 2 A65044 43 103.5 17.7 649 2 T18063 44 102 17.5 430 2 JC2301 45 102 17.5 449 2 S16748 proline-rich prote

C; Keywords: disulfide bond; immunoglobulin

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thrombospondin 4 - African clawed frog
C;Species: Xenos laevis (African clawed frog)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: A45441
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A;Molecule type: mRNA
A;Residues: 1-961 <LAW>
A;Cross-references: EMBL:Z19585; NID:g311625; PIDN:CAA79635.1; PID:g311626
A;Cross-references: EMBL:Z19585; NID:g311625; PIDN:CAA79635.1; PID:g311626
                                                                                                                              A, Title: Identification and A; Reference number: A45441; A; Accession: A45441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Lawler, J.; McHenry, K.; Duquette, M.; Derick, L.
J. Biol. Chem. 270, 2809-2814, 1995
A;Title: Characterization of human thrombospondin-4.
A;Reference number: A55710; MUID:95155352; PMID:7852353
A;Accession: A55710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 11-Aug-1995 #text_change 13-Aug-1999
C;Accession: A55710; S36069
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A; Cross-references: GB:Z19091; NID:g288777; PIDN:CAA79518.1; A; Note: sequence extracted from NCBI backbone (NCBIN:124858;
                                                     A;Molecule type: nucleic acid
A;Residues: 1-955 <LAW>
                                                                                                                                                                                                    R;Lawler, J.; Duquette, M.; Whittaker, C.A.; Adams, J.C.; McHenry, K.; DeSimone, J. Cell Biol. 120, 1059-1067, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Description: participates in cell migration and adhesion, C;Superfamily: thrombospondin 3; EGF homology
                                                                                                   A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position: 1q21-1q23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GDB:463011; OMIM:600715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;14-62/Disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Keywords: beta-hydroxyasparagine; beta-hydroxyaspartic acid; calcium binding;; 1-21/Domain: signal sequence #status predicted <SIG>; 22-961/Product: thrombospondin 4 #status predicted <MAT>; 290-324/Domain: EGF homology <EGF1>; 390-324/Domain: EGF homology <EGFP>; 330-362/Domain: EGF homology <EGFP>; 330-362/Domain: EGF homology <EGFP>; 330-362/Pomain: EGF homology <EGFP>; 330-362/Pomain: EGF homology <EGFP>; 303/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted ; 343/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted ; 343/Modified site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLGPQMLRELQETNAALQDVRDWLRQQVREITFLKNTVMECDACGP----QPQPKPQPQP 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bonds:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.9%; Score 145.5; DB 1; 42.9%; Pred. No. 3.6e-05; tive 10; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25.0%;
96.2%;
                                                                                                                                                      characterization of thrombospondin-4, MUID:93163109; PMID:8432726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human
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Pred. No. 4.8e-06;
0; Mismatches 1
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  PID: 9288778
NCBIP: 124860)
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                                                                                                                                                                                 member of the
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                                                                                                                                                                                                                                     D.W.
circumsporozoite protein precursor - P
N;Alternate names: sporozoite surface
C;Species: Plasmodium berghei
C;Date: 30-Jun-1991 #sequence_revision
                                                                                                   RESULT
OZZQBK
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A;Molecule type: DNA
A;Rosidues: 1-26, I', 28-68, 'PMLRR', 75-126, 'P', 128-134, 'PpPNANDP', 135-332 <EIC>
A;Cross-references: GB:M14135, NID:g160245, PION:AAAA29577.1; PID:g160246
A;Cross-references: GB:M14135, NID:g160245, PION:AAAA29577.1; PID:g160246
R;Weber, J.L.; Egan, J.E.; Lyon, J.A.; Wirtz, R.A.; Charoenvit, Y.; Maloy, W.L.
Exp. Parasitol. 63, 295-300, 1987
A;Title: Plasmodium berghes: cloning of the circumsporozoite protein gene.
A;Reference number: S13446; MUID:87218962; PMID:3556207
A;Accession: S13446
                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 61-122,'A',124-332 <WEB>
A;Residues: 61-122,'A',124-332 <WEB>
A;Cross-references: GB:M25445; NID:g160177; PIDN:AAA29531.1; PID:g160178
C;Comment: There are three distinct regions in the mature circumsporozoite obic membrane-anchoring sequence.
c)Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homol c;Keywords: sporozoite; surface antigen; tandem repeat
c)Keywords: sporozoite; surface antigen; tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              circumsporozoite protein precursor - Plasmodium berghei (strain N;Alternate names: sporozoite surface antigen C;Species: Plasmodium berghei C;Date: 30-Sep-1987 #sequence_revision 28-Jul-1995 #text_change C;Accession: A44948; A25083; S13446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Title: Circumsporozoite protein of Plasmodium berghei: A;Reference number: A25083; MUID:87089740; PMID:2432395 A;Accession: A25083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol. Biochem. Parasitol. 39, 151-154, 1990
A; Title: Sequence of the circumsporozoite gene of Plasmodium A; Reference number: A44948; MUID:90158693; PMID:2406593
                                                                                                                                                                                                                    F;258-310/Domain: thrombospondin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:M28887
R;Elchinger, D.J.; Arnot, D.E.; Tam, J.P.; Nussenzweig,
Mol. Cell Biol. 6, 3965-3972, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A44948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
                                                                                                                                                                                                                                       ;24-332/Product: circumsporozoite
;94-189/Region: 8-residue repeats
;199-230/Region: 2-residue repeats
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                                                                                                                                                                                                                                                                                            ;1-23/Domain: signal sequence #status predicted <SIG>
;24-332/Product: circumsporozoite protein #status predicted <MAT>
                                                                                                          Matches
                                                                                                                                        Query Match
Best Local
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Best Local
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37; Conserv
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                                                                                                                                   Similarity
                              PQPQPKPQPQPQPQPKPQPKPEPEGTGSSEKD 107
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  PQPQPQPQPQPQPQPRPQPQPQPGGNNNNKNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEAGQQTGDVSRQLIGQITQMNQMLGELRDVMRQQVKETMFLRNTIAECQACGLGPDFPL
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                                                                                                                                                                                                                                          2-residue repeats
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Pred. No. 0.00015;
                                                                                                                                                                                                              type 1 repeat homology <THR1>
                                                                                                                                   Score 133;
Pred. No. 0.
                                                                                                          Mismatches
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240
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                                                                                                                                                         Length 332;
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30-Jun-1991 #sequence_revision

Plasmodium

berghei (strain

ANKA

clone

antigen

30-Jun-1991 #text_change

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J. Gen. Virol. 69, 1531-1574, 1988

A,Title: The complete DNA sequence of the long unique region in the A,Reference number: A30083; MUID:88274327; PMID:2839594

A,Accession: 130085
                          C;ACCession: Allow, L.; Ruiz-Lozano, P.; Yang, Q.; Chien, R;Cao, L.; Zhang, L.; Ruiz-Lozano, P.; Yang, Q.; Chien, J. Biol. Chem. 273, 21077-21083, 1998
A;Title: A novel putative protein-tyrosine phosphatase c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Nucleotide sequence of the Plasmodium berghei A;Reference number: S07873; MUID:90221834; PMID:2183186 A;Accession: S07873
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Nucleic Acids Res. 18, 376, 1990
               A;Reference number: Z18004; MUID:98361981; A;Accession: T14355
                                                                                                     C; Accession:
                                                                                                                                         protein-tyrosine-phosphatase (EC 3.1.3.48) TD14 - rat
C;Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                               RESULT 8
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A;Residues: 1-3164 <
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A;Residues: 1-59,'I',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, A,Reference number: $12571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Lockyer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-348 <LOC>
                                                                                               ;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999;Accession: T14355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 protein - human herpesvirus 1 (strain Species: human herpesvirus 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;21-348/Product: circumsporozoite protein #status
;94-205/Region: 8-residue repeats
;215-247/Region: 2-residue repeats
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Cross-references: EMBL:X17006; NID:99784; PIDN:CAA35608.1;
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Best Local
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preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                        h 22.6%;
Similarity 66.7%;
22; Conservative
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                                                                                                                                                                                                                                                                         TVMECDACGPQPQPKPQPQPQPQPKPQPKPEPE 99
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Pred. No. 0.00017;
8; Mismatches 4
                                                                                                                                                                                                                                                                                                                        Score 132; DB 1; Length 3164; Pred. No. 0.0017; Indels 5; Mismatches 6; Indels
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                                                                                    K.R.; Graham, R.M.;
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A;Molecule type: mRNA
A;Residues: 1-1494 <CAO>
A;Cross-references: EMBL:AF077000; NID:g3598973; PID:g3598974;
A;Experimental source: brain
C;Genetics:
A;Gene: PTP-TD14
C;Function:
                                                                                                                                                                                                                                                                                                                     hypothetical protein T04F8.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PQ-rich protein - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Description: may be involved in regulating C;Keywords: phosphoric monoester hydrolase
                                                                                                                                                                                                                                                           submitted to the EMBL Data A; Reference number: Z19895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-400 < WAG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A; Accession: S58222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, July 1995 A;Description: A cDNA, which predicts a protein with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: S58222
R;Wagner, F.F.; Flee
                                                                                                      A; Introns:
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                                                                                                                                                                                                                                           A; Accession: T24470
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                                                                                                                                                                                                                           Status: preliminary; translated
                                                         Query Match
Best Local Similarity
                                                                                                                      Map position:
                                                                                                                                     Gene: CESP:T04F8.8
                                                                                                                                                                 Experimental source:
                                                                                                                                                                   ;Cross-references: EMBL:Z66565; P
;Experimental source: clone T04F8
                                                                                                                                                                                                                                                                                                          Accession:
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Best Local (
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Pred. No. 0.
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Pred. No. 0.0043;
                                                         Score 118;
Pred. No. 0
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                                         Mismatches
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                                              1.0017;
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108 PEPEPRPEPQPEPQPEPQPE 131

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R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Fgasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7

A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: C91067
      A;Title: Complete genome sequence of Pseudomonas aeruginosa A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Accession: F83634
                                                                  R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, .; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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A; Accession: T17557
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A; Residues: 1-422 < HAY>
                                                                                                                                                                                                               hypothetical protein PA0081 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                            F83634
                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   procyclin homolog A67R - Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:BA000007; PIDN:BAB36930.1; PID:g13362978; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: C91067
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Best Local S
Matches 17
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(Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96435.1; Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96435.1
                                                                                                                                                               Species: Pseudomonas aeruginosa;Date: 15-Sep-2000 #text_change 31-Dec-2000;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                    Accession:
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                                                                                                                                                                                                                                                                                                                              EPSPEPSPEPSPEPSPEPTPSPE
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Pred. No. 0.0038;
8; Mismatches 25
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A; Status: preziment,
A; Molecule type: DNA
A; Residues: 1-497 CSTO>
A; Residues: 1-497 CSTO>
A; Cross-references: GB: AE004447; GB: AE004091; NID: g9945902; PIDN: AAG03471.1; GSPDB: GN001:
A; Cross-referental source: strain PAO1
A; Experimental source: strain PAO1
                                                                                                                                                                                              C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 21-Jan-2000 C;Accession: E64687
C;Accession: E64687
R;Tomb, J; F; White, O; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.N. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: E64687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Variety: strain J99
C; Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 21-Jan-2000 C; Accession: F71829
R; Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vature 397, 176-180, 199
A; Title: Genomic sequence comparison of two unrelated isolates of the human A; Reference number: A71800; MUID:99120557; PMID:9923682
A; Accession: F71829
                                                                                    A; Molecule type: DNA
A; Residues: 1-285 < TOM>
A; Cross-references: GB: J
C; Superfamily: tonB prof
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C;Superfamily:
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A;Residues: 1-280 <ARN>
A;Ross-references: GB:AE001549; GB:AE001439; NID:g4155858; PIDN:AAD06833.1; PID:g4155861
A;Experimental source: strain J99
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Search completed: August 26, 2003, 16:05:21 Job time: 51.1947 secs

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Copyright (c) 1993 - 2003 Compugen Ltd.
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SUMMARIES

Result No.	Score 262.5 234	Query Match 44.9 40.1	Length 757 755	1 1 1	ID COMP HUMAN COMP RAT TSP4 HUMAN	Description
ں ∡ہ			086 196	- -	TSP4_RAT	P3544 P4974
IJ	138.5	23.7	955	μ.	TSP4_XENLA	Q0644
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7	133	22.8	347	-	CSP_PLABA	P2309
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9	117	٠	220	۳	NOL3 MOUSE	0×tp60
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12	112.5	19.3	839	- •	TRA9 MAIZE	P030
13	111		115	ш	PARX_TRYBB	P14043
14	111	19.0	129	μ,	PARB TRYBB	P0979:
15	111	•	143	_	PAR1_TRYBB	P08469
16	111	•	145	ш	PARC_TRYBB	Q06084
17	111	٠	221	_	NOL3_RAT	Q62881
18	111	•	806	,	TRA1 MAIZE	P08770
19	108		722	-	Z219 HUMAN	Q9p2y4
20	107	٠	613	μ.	PKPA_PHYBL	Q01577
21	104		1569	ш	YPJA_ECOLI	P52143
22	102	7.	449	μ.	APG BRANA	P40603
23	101	7.	342	<u>, , , , , , , , , , , , , , , , , , , </u>	TONE PSEAE	Q5136
24	101	.7	450	_	V50K_BYDVP	P09516
25	101	7.	565	_	MOT8 MOUSE	07032
26	100.5	17.2	956	-		P49746
27	100	7.	643	ب	VP40_HSVE2	P5236
28	100	7.	956	ᆫ		20589
29	99	17.0	1493	۳		Q6292
30	99	7.	1520		ACFD_ECOLI	. Q46837
31	98	٥.	534	۳.		P40602
32	97	٥.	243	ب	TONB KLEPN	P45610
33	96.5	16.5	737	ᆫ		Q9r1d
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Q9pr99 u	Q92794 ho	Q06670 aı	P29536 h	P45508 es	P18627 h	Q9h161 ho	P46383 er	P03251 ht	P13916 gl	Q91ye5 m	P36021 hc
ureaplasma	homo sapien	utographa	omo sapien	scherichia	omo sapien	omo sapien	nterobacte	uman adeno	lycine max	us musculu	homo sapien

ALIGNMENTS

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NAT MED INE=9732 INE=	SEQUENCE FROM N.A. TISSUB-Cartilage; MEDLINE=95229140; PubMed=7713493; Newton G., Weremowicz S., Morton C.C., Copeland N.G., Gilbert D.J., Jenkins N.A., Lawler J.; "Characterization of human and mouse cartilage oligomeric matrix protein."; Genomics 24:435-439(1994). [2] VARIANTS PSACH SER-459 DEL; TYR-468 AND TYR-472. WEDLINE=95400301; PubMed=7670471; Hecht J.T., Nelson L.D., Crowder E., Wang Y., Elder F.F.B., Harrison W.R., Francomano C.A., Prange C.K., Lennon G.G., Deere M., Lawler J.; "Mutations in exon 17B of cartilage oligomeric matrix protein (COMP) cause pseudoachondroplasia."; Nat. Genet. 10:325-329(1995). [3] VARIANTS MED TYR-342, AND VARIANT PSACH ARG-328. MEDLINE=95400302; PubMed=7670472; Nat. Genet. 10:325-329(1995). [4] VARIANTS MED TYR-342, AND VARIANT PSACH ARG-328. MEDLINE=95400302; PubMed=7670472; Cekleniak J.A., Knowlton R.G., Cohn D.H.; "Pseudoachondroplasia and multiple epiphyseal dysplasia due to mutations in the cartilage oligomeric matrix protein gene."; Nat. Genet. 10:330-336(1995). Nat. Genet. 10:330-336(1995).	_HUMAN

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EMBL; L32137; AAA572531; -...

EMBL; S79499; AAB35269.1; -...

EMBL; S79500; AAB35270.1; -...

HSSP; P35444; IUDF:

Genew; HGNC:2227; COMP.

MIM; 600310; -...

MIM; 132400; -...

MIM; 171710; -...

MIM; 171710; -...

GO; GO:0005578; C:extracellular GO; GO:0005509; F:cxlclum ion bi GO; GO:0005509; F:extracellular GO; GO:0005201; F:extracellular GO; 
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VARIANTS PSACH AND MED.
WARLINE=98130533; PubMed=9463320;
MEDLINE=98130533; PubMed=9463320;
Briggs M.D., Mortier G.R., Cole W.G., /
Bonaventure J., Nuytinck L., de Paepe
Bonaventure J., Nuytinck L., de Paepe
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Hum. Genet
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Loughlin J., Irven C., Mustafa Z., Briggs M.D., Carr A., Lynch S
Knowlton R.G., Cohn D.H., Sykes B.;
"Identification of five novel mutations in cartilage oligomeric
matrix protein gene in pseudoachondroplasia and multiple epiphy:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-98112442; PubMed-9452063;
Susic S., Ahier J., Cole W.G.;
"Pseudoachondroplasia due to the substitution of the highly conserved
Asp482 by Gly in the seventh calmodulin-like repeat of cartilage
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Ikegawa S., Ohashi H., Nishimura G., Kim K.C., Sannohe A.,
Ikegawa S., Pukushima Y., Nagai T., Nakamura Y.;
Ikimizuka M., Pukushima Y., Nagai T., Nakamura Y.;
"Novel and recurrent COMP (cartilage oligomeric matrix protein)
mutations in pseudoachondroplasia and multiple epiphyseal dysplasia.";
Hum. Genet. 103:633-638(1998).
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                                                                                                                       GO:0005578; C:extracellular matrix; TAS.
GO:0005509; F:calcium ion binding activity; TAS.
GO:0005201; F:extracellular matrix structural constituent;
GO:0007397; P:histogenesis and organogenesis; TAS.
GO:0001501; P:skeletal development; TAS.
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A., Leroy J.G., Biesecker L.,
Rimoin D.L., Knowlton R.G.,
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PROSITE; PS00122; EGF_1; FALS
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01187; EGF_CA; 2.
Glycoprotein; Cell adhesion;
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INTERCHAIN (PROBABLE).

BY SIMILARITY.

BY SIMILARITY.
                                                                                                                                       /FTId=VAR 007617.
D -> V (IN PSACH; MILD FORM).
/FTId=VAR 007618.
D -> V (IN MED; FAIRBANK TYPE:
/FTId=VAR 007619.
D -> Y (IN MED).
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EGF-LIKE 3.
EGF-LIKE 3.
EGF-LIKE 4.
TSP TYPE-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARTILAGE OLIGOMERIC N-TERMINAL.
                             /FTId=VAR_007624.
C -> G (IN PSACH; MILD FORM)
                                               /FTId=VAR 007622.
MISSING (IN PSACH).
/FTId=VAR 007623.
MISSING (IN PSACH; MILD FORM)
                                                                                                       /FTId=VAR_007621
          /FTId=VAR_007625
PNSD -> V (IN PS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                 FTId=VAR 007620.
                                                                                                                                                                                                                /FTId=VAR_007616
                                                                                                                                                                                                       -> Y (IN MED;
                                                                                              (IN MED;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7554321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CALCIUM-BINDING CALCIUM-BINDING
          PSACH).
                                                                                             FAIRBANK TYPE).
                                                                                                                                                             FAIRBANK TYPE)
                                                                                                                                                                                                       FAIRBANK TYPE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MATRIX PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
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RESULT 2
COMP RAT
ID P354
AC P355
DT 01-15
RN (CB)
RN 
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Best Local S
Matches 57
                                                                      InterPro; IPR001881; EGF Ca.
InterPro; IPR006209; EGF like.
InterPro; IPR003367; tsp_3.
Pfam; PF000008; EGF; 1.
Pfam; PF002412; tsp_3; 9.
SMAXT; SM00179; EGF CA; 2.
PROSITE; PS00122; EGF 1; FALSE_NEG.
PROSITE; PS01186; EGF CA; 2.
PROSITE; PS01187; EGF CA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Cartilage;
TISSUE=Cartilage;
MEDLINE=93054522; PubMed=1429587;
MEDLINE=93054522; PubMed=1429587;
Oldberg A., Antonsson P., Lindblom K., Heinegaard D.;
"COMP (cartilage oligomeric matrix protein) is structurally to the thrombospondins.";
To the thrombospondins.";
Thiol. Chem. 267:22346-22350(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMP RAT
P35444;
01-JUN-1994
01-JUN-1994
15-SEP-2003
Signal; 3D-structure.
SIGNAL 1 1
CHAIN 20 75
                                                                                                                                                                                                                                                       EMBL;
PIR; A
PDB; 1
PDB; 1
                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 274:761-765(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The crystal structure of a five-stranded coiled coil in COMP: prototype ion channel?";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Engel J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97020114; PubMed=8864111; Malashkevich V.N., Kammerer R.A., Efimov V.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cartilage oligomeric
                                                          Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY. SIMILARITY: Contains 4 EGF-like domains. SIMILARITY: Contains 7 TSP type-3 domains.
                                                                                                                                                                                                                                                   ; X72914; CAA51419.1;
A44315; A44315.
1VDF; 08-OCT-97.
1FBM; 09-AUG-00.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89
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57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VMECDACGPQ-----PQPKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VMECDACGMOOSVRTGLPSVRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 29,
(Rel. 29,
(Rel. 42,
                                                        Cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence upoacc,
Last annotation update)
---ix protein precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 262.5; DB 1;
Pred. No. 2.7e-15;
                                                      Calcium-binding;
POTENTIAL.
CARTILAGE OLIGOMERIC MATRIX PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; E
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     755
                                                        Repeat; EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (COMP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schulthess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi; 
; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     related
                                                        domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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RESULT 3
TSP4 HW
ID TSP4 H
AC P35443
DT 01-JUN
DT 01-JUN
DT 28-FEB
DE Thromb
GN THBS4 H
OS HOMO S
GN HOMO S
GN HOMO S
GN HOMO S
HOMO S
GN HOMO S
G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; P
NCBI TaxID=9606;
                                                                                                                                                                                                              01-JUN-1994
01-JUN-1994
28-FEB-2003
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DISULFID
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P35443;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HELIX
                                                                                                                                                                    Thrombospondin 4 precursor THBS4 OR TSP4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                        TISSUE=Heart
                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
  MEDLINE=93353522; PubMed=8350346;
                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                               83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 LIALAAVCSAAKKGSSLGGDCCSDLGPQMLRELQETNAALQDVRDWLRQQVREITFLKNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               VMECDACGPQPQPKPQPQPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLALAALRATGQGQIPLGG----DLAPQMLRELQETNAALQDVRELLRHRVKEITFLKNT
                                                                                                                                                                                                                                                                                                                                                                                                     VMECDACGMOPARTPGLSVRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30
67
69
755
                                                                                                                                                                                                          (Rel. 29, Created)
(Rel. 29, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA,
                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82663 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 234; DB
; Pred. No. 7.3e
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERCHAIN.
INTERCHAIN.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-TERMINAL.

RGF-LIKE 1.

EGF-LIKE 2. CA

EGF-LIKE 3. CA

EGF-LIKE 4.

TSP TYPE-3 1.

TSP TYPE-3 2.

TSP TYPE-3 3.

TSP TYPE-3 3.

TSP TYPE-3 5.

TSP TYPE-3 5.

TSP TYPE-3 5.

TSP TYPE-3 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C-TERMINAL
                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AB48888FE093C598 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       85
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                                                                                                                                                                                                                                                                                                  961
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                  B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3e-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.
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DR EMBL; Z19585, CAA79635.1; -.

DR HSSP; P35444; 1VDF.

DR HSSP; P35444; 1VDF.

DR Genew; HGNC:11788; THBS4.

DR GO; GO:0005578; C:extracellular matrix; TAS.

DR GO; GO:000559; F:calcium ion binding activity; TAS.

DR GO; GO:000590; F:calcium ion binding activity; TAS.

DR GO; GO:0005930; P:substrate-bound cell migration, cell extension; TAS.

DR GO; GO:0006930; EGF_like.

DR InterPro; IPR003167; tsp_3.

DR InterPro; IPR003167; tsp_3.

DR InterPro; IPR003167; tsp_3.

DR InterPro; IPR003167; tsp_3.

DR Ffam; PF00412; tsp_3; 9.

DR Pfam; PF02412; tsp_3; 9.

DR Pfam; PF02412; TSPN, 1.

DR Pfam; PF02510; TSPN, 1.

DR Pfam; PF02717; EGF_CA; 2.

DR SMART; SM00179; EGF_CA; 2.

DR PROSITE; PS001186; EGF_2; 1.

DR PROSITE; PS01186; EGF_2; 1.

DR PROSITE; PS01186; EGF_2; 1.
   SIGNAL
CHAIN
CHAIN
DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lawler J., Duquette M., Urry L., McHenry K., Smith T.F.;
"The evolution of the thrombospondin gene family.";
"Mol. Evol. 36:509-516(1993)"
-i- FUNCTION: ADHESIVE GLYCOPROTEIN THAT MEDIATES CELL-TO-CELL AND CELL-TO-MATRIX INTERACTIONS. CAN BIND TO FIBRINGEN, FIBRONECTIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lawler J., Duquette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CELL-TO-MATRIX INTERACTIONS. CAN BIND TO FIBRINGEN, LAMININ AND TYPE V COLLAGEN.
SUBUNIT: Homotrimer; disulfide-linked.
SIMULARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.
SIMILARITY: Contains 4 EGF-like domains.
SIMILARITY: Contains 7 TSP type-3 domains.
SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
     adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tatement is not removed. Usage by and for commercial license agreement (See http://www.isb-sib.ch/announce/
EGF-LIKE 1.

EGF-LIKE 2, CALCIUM-BINI
EGF-LIKE 3, CALCIUM-BINI
EGF-LIKE 4.

TSP TYPE-3 1.

TSP TYPE-3 2.

TSP TYPE-3 3.

TSP TYPE-3 5.

TSP TYPE-3 7.

TSP TYPE-3 7.

TSP TYPE-3 7.

TSP TYPE-3 7.

C-TERMINAL.

CELL ATTACHMENT SITE (PC INTERCHAIN (PROBABLE).

INTERCHAIN (PROBABLE).

INTERCHAIN (PROBABLE).

BY SIMILARITY.

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
THROMBOSPONDIN
N-TERMINAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Calcium-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                 CALCIUM-BINDING CALCIUM-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.
                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGF-like domain;
                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
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TRESULT 4
TREP4 PATE
TO 11-CT
TO TO 11-CT
TO THESE
ON RATE
THESE
ON RATE
ON MANDIA
THESE
ON MADDIA
THESE
ON MADDIA
THESE
ON THESE
TO 11-CT
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Best Local S
Matches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Thrombology of the contains o
HSSP; P35444; IVDF.
InterPro; IPR001881; E
InterPro; IPR006209; F
InterPro; IPR003367; t
InterPro; IPR003129;
Pfam; PF000008; EGF; 2;
Pfam; PF02412; tsp_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSP4_RAT STANDARD; PRT; 980 AA P49744; O1-OCT-1996 (Rel. 34, Created) O1-OCT-1996 (Rel. 34, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=Lewis; TISSUE=Skeletal muscle;
MEDLINE=96074771; PubMed=7490284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thrombospondin 4 precursor. THBS4 OR TSP4 OR TSP-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arber S., Caroni P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
                                                                                                                                                                              X89963; CAA62002.1;
P35444; IVDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            278
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                                                             EGF_Ca.
EGF_like.
tsp_3.
TSPN.
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N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
MW; 55A48AF481AEE9DD C
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Pred. No. 3.4e
10; Mismatches
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Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   matrix protein expressed in promotes neurite outgrowth.
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1es 25;
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RESULT 5
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ID TSP4 X
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DE Thromb
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OC Eukary
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Best Local S
Matches 29
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SMART; SM00179; EGF CA; 2.
SMART; SM00210; TSPN; 1.
PROSITE; PS00022; EGF 1; FA
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01187; EGF CA; 2
                          TSP4 XENLA
Q06441;
Q1-JUN-1994
Q1-JUN-1994
28-FEB-2003
                                                                                                                                                                                                                    DISULFID
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        01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Thrombospondin 4 precursor.
Xenopus laevis (African clawed frog).
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SIGNAL
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein;
                                                                                                                                                236
                                                                                                                                                                                            Similarity
                                                                                                            APPAPPTRP
                                                                                                                                                         DLGPQMLRELQETNAALQDVRDWLRQQVREITFLKNTVMECDACGPQPQPKPQPQ---PQ
                                                                                                                                             DFNRQFLGQMTQLNQLLGEVKDLLRQQVKETSFLRNTIAECQACGPLSFQSPTPNTLVPI
                                                                                                                             PQPKPQPKP 96
                                                                                                                                                                                                                     AA;
                                                               STANDARD;
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                                                                                                                                                                                                                                       adhesion;
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                                                                                                                                                                                                                      WW.
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                                                                                                                                                                               Score 144.5; ub .,
pred. No. 4.2e-05;
pred. No. 4.2e-05;
                                                                                                                                                                                                                            INTERCHAIN (PROBABLE)
INTERCHAIN (PROBABLE)
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGF-LIKE 1.

EGF-LIKE 3.

EGF-LIKE 4.

TSP TYPE-3 7

TSP TYPE-3 7

TSP TYPE-3 3

TSP TYPE-3 5

TSP TYPE-3 5

TSP TYPE-3 5

TSP TYPE-3 6
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N-TERMINAL.
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                            on update)
                                                               955
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                                                                                                                                                                                                                     CRC64;
                                                                                                                                                                                                 Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain;
                                                                                                                                                                                 Gaps
                                                                                                                                                                87
 InterPro; IPR001881; EGF_Ca.
InterPro; IPR006209; EGF_like.
InterPro; IPR003107; tsp_3.
InterPro; IPR003129; TSN.
Pfam; PP000008; EGF_; 2.
Pfam; PP02210; TSN; 1.
SMART; SM00179; EGF_CA; 2.
SMART; SM00179; EGF_CA; 2.
SMART; SM00210; TSN; 1.
PROSITE; PS001286; EGF_2; 1.
PROSITE; PS001186; EGF_CA; 2.
PROSITE; PS01186; EGF_CA; 2.
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Glycoprotein
Signal.
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                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                          PIR; A45441; A45441.
                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lawler J., Du
Desimone D.W.
                                                                                                                                                                                                                                                                                                                                                 HSSP;
                                                                                                                                                                                                                                                                                                                                                 P35444; 1VDF
                                                                                                                                                                                                                                                                                                                                                                  Z19091; CAA79518.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163109; PubMed=8432726;
Duquette M., Whittaker
 adhesion;
C-TERMINAL.
INTERCHAIN (PRO
INTERCHAIN (PRO
INTERCHAIN (PRO
BY SIMILARITY
                                                                                        N-TERMINAL

EGF-LIKE 1.

EGF-LIKE 3.

EGF-LIKE 3.

EGF-LIKE 4.

TSP TYPE-3 2

TSP TYPE-3 3

TSP TYPE-3 3

TSP TYPE-3 4

TSP TYPE-3 4

TSP TYPE-3 6

TSP TYPE-3 7
                                                                                                                                                                                                                             Calcium-binding; Repeat;
                                                                                                                                                                                                   THROMBOSPONDIN
                                                                                                                                                                                                           POTENTIAL
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                                                              (PROBABLÉ).
                                                                                          7654321
                                                                                                                                                                CALCIUM-BINDING CALCIUM-BINDING
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Δ.

(POTENTIAL)

EGF-like domain;

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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Kenopodinae; Xenopus.
NCBI_TaxID=8355;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Identification and characterization of thrombospondin-4, a new member of the thrombospondin gene family.";
J. Cell Biol. 120:1059-1067(1993).

J. Cell Biol. 120:1059-1067(1993).

-i- FUNCTION: ADHESIVE GLYCOPROTEIN THAT MEDIATES CELL-TO-CELL AND CELL-TO-MATRIX INTERACTIONS. CAN BIND TO FIBRINGGEN, FIBRONECTIN, LAMININ AND TYPE V COLLAGEN, MAY PARTICIPATE IN THE GENESIS AND FUNCTION OF CARDIAC AND SKELETAL MUSCLE.

-i- SUBUNT: Homottimer; disulfide-linked.

-i- SUBUNT: Homottimer; disulfide-linked.

-i- COLLAGEN: INITIAL EXPRESSION DURING NEURULATION.
INCREASE DURING TAILBUD STAGES BUT DECREASE BY THE FEEDING TADPOL
the European Bioinformatics Institute. The use by non-profit institutions as long of modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                              -i- SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.
-!- SIMILARITY: Contains 4 EGF-like domains.
-!- SIMILARITY: Contains 7 TSP type-3 domains.
-!- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
                                                                                                             SWISS-PROT entry is copyright. It is produced through a collab-
een the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
                                             (See http://www.isb-sib
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NÉURULATION.
THE FEEDING TADPOLE
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BL outstation -
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Best Local
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CSP_PLABE
P06915;
01-JAN-1988
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  PRINTS;
SMART; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE-87089740; PubMed-2432395;

Eichinger D.J., Arnot D.E., Tam J.P., Nussenzweig

"Circumsporozoite protein of plasmodium berghei: g
identification of the immunodominant epitopes.";

Mol. Cell. Biol. 6:3965-3972(1986).
                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium berghei.
Eukaryota; Alveolata;
NCBI_TaxID=5821;
                    InterPro; IPRO03067; Crcmsprzoite.
InterPro; IPRO03084; TSP1.
Pfam; PF00090; tsp 1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
                                                                                                                   EMBL; M14135; AAA29577.1; -. PIR; A44948; OZZQMB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Circumsporozoite protein
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01-JAN-1988 (Rel. 06,
28-FEB-2003 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                           send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF TH MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
                                                                                                                                                                                                                                                                                                                                                                             VERTEBRATE HOST).

MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.

SIMILARITY: Contains 1 TSP type-1 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23
  ; PR01303; CRCM
SM00209; TSP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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955 AA;
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34.3%;
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Last annotation updat
ein precursor (CS).
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Pred. No. 0.00013;
3; Mismatches 31;
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CRC64;
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cloning a
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RESULT 7
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Best Local :
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Best Local
                                                                                                                                                                                                                                                                              EMBL; X17606; CAA35608.1; -.
pIR; S07873; OZZQBK.
InterPro; IPRO03067; Crcmsprzoii
InterPro; IPR000884; TSP1.
Pfam; PF00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P23093;
01-NOV-1991
01-NOV-1991
28-FEB-2003
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Malaria;
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SEQUENCE
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con entities requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE=90221834; PubMed=2183186;
Lockyer M.J., Davies C.S., Suhrbier A., Sinden R.E.;
Lockyer M.J., Davies C.S., Suhrbier A., Sinden R.E.;
"Nucleotide sequence of the Plasmodium berghei circumsporozoite
protein gene from the ANKA clone 2.34L.";
Nucleic Acids Res. 18:376-376(1990).
-I- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT
SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE
MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Circumsporozoite protein precursor (CS).
Plasmodium berghei (strain Anka).
Eukaryota; Alveolata; Apicomplexa; Haemo
                                                                                                                                                                                                                             PROSITE; PS50092; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced throubetween the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -I- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBA
ANCHORING THE PROTEIN TO THE CELL MEMBRANE. T
WOULD BE THE SURFACE ANTICEN OF THE ORGANISM.
-I- SIMILARITY: Contains 1 TSP type-1 domain.
                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=5823;
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Sporozoite; Repea
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(Rel. 20, Last sequence up
(Rel. 41, Last annotation
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                    22.8%;
62.5%;
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                                                                                                                          :; Signal.

POTENTIAL.

CIRCUMSPOROZOITE PROTEIN.

13 X 8 AA REPEATS.

17 X 2 AA REPEATS OF P-Q.
Score 133; DB
Pred. No. 0.00
8; Mismatches
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PROBABLE.
CIRCUMSPOROZOITE
                                                                                                             TSP
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16 X 2 AA TANDEM
TSP TYPE-1.
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Pred. No. 0
                                                                                       OEC240EE35681AF8 CRC64;
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                                                                                                               TYPE-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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                                            DB 1;
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Best Local S
Matches 22
                                                                                                                                                                                                                                                                                 NOL3 MOUSE
Q9D1X0;
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=C57BL/6J; T
                                                                                                                                                                                                        28-FEB-2003 (Rel. 41,
28-FEB-2003 (Rel. 41,
28-FEB-2003 (Rel. 41,
Nucleolar protein 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it the European Bioinformatics Institute. There are no restrictions on it uses, by non-profit institutions as long as its content is in no was used, by non-profit institutions as long as its content is in no was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McGeoch D.J., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C., McNab D., Perry L.J., Scott J.E., Taylor P., "The complete DNA sequence of the long unique region in the genom
                                                                                                                                                                                     NOL3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro, IPR006928, Herpes teg N.
InterPro, IPR005210, Herpes UL36.
Pfam; PF04843, Herpes teg N; 1.
Pfam; PF03586; Herpes_UL36; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X14112; CAA32311.1; -. PIR; I30085; WMBEH6.
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-1989
01-APR-1993
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P10220;
                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 TVMECDACGPQPQPKPQPQPQPQPKPQPKPEPE 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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(Rel. 10,
(Rel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                          (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            el. 10, Last sequence update) el. 25, Last annotation update) protein (Virion protein UL36).
                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA,
TISSUE=Adipose tissue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2980
                                                                                                    Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35 X 2 AA TANDEM REPEATS OF P-Q.
335857 MW; CC5D31FF4F9FE3F4 CRC64;
                                                                                                                                                                                                                                   Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                    Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 132; DB 1;
Pred. No. 0.0016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 0.00
5; Mismatches
                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                          220
                                                                                                                                                                                                                                update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 3164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a collaboration
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                                                                                                                                                                                                                                          TONB_HELPJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RA Kawai J. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Pukuda S.,
RA Airawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Ra Asitowa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Ra Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomata M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomata M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Rasaki K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Rasaki W., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Rasaki W., Okido T., Furuno M., Aono H., Bararaelli R.,
Romanstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Rusaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Rasaki H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Rayashi R., Sato K., Schoenbach C., Seya T., Shabata Y., Storch K.-F.,
Rayashi R., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Rayashi R., Sato K., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 31
                                                                                                                                               Q9ZJP4;
16-OCT-2001
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:1925938; Nol3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                    Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
                                                                                                            TONB OR JHP1260.
                                                                                                                                                                                                                          TONB HELPJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nuclear protein; mRNA splicing.

DOMAIN 4 95 CARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: May be involved in RNA splicing (By similarity).
-!- SUBUNIT: Interacts with SRp30c, NPM1, CASP2, CASP8 and CED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hayashizaki Y.;
                             NCBI_TaxID=85963;
                                                     Helicobacteraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity)
                                                                                                                                                                                                                                                                                                                     173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ro; IPR001315; CARD.
SM00114; CARD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                     TVMECDACGPQPQPKPQPQPQPQPKPQPKPEPEGTGSSEKD 107
                                                                                                                                                                                                                                                                                                                                                                                                GTTCPELPRASEQEEVGGPEGSEALQPRTPEEPELEAEATEGDEPD-LEQEM---
                                                                                                                                                                                                                                                                                                                                                                                                                                   GDCCSDL-----GPQMLRELQ-----
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                                                                                                                                             (Rel. 40, Created)
(Rel. 40, Last seq
(Rel. 40, Last ann
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                                                                                                                                                                                                                          STANDARD;
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24567 MW;
                                                       Helicobacter
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                                                                                                                                             sequence update) annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
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                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A4DCD57C1EB320A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                               update)
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SEQUENCE FROM N.A

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RESULT
TONB_H
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Best Local S
Matches 18
[1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=26695 / ATCC 700392;
STRAIN=26695 / ATCC 700392;
STRAIN=97394467; PubMed=9952185;
MEDLINE=97394467; PubMed=9952185;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty Fleischmann R.D., Ketchum K.A., Klrkness E.F., Peterson S., Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Nelson K., Quackenbush J., Dodson R., Khalak H.G., Glodek A.,
                                                                                                                                                                                                                                                                                  TONB HELPY
025899;
15-DEC-1998
15-DEC-1998
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";

Nature 397:176-180(1999).

-i- FUNCTION: INTERACTS WITH OUTER MEMBRANE RECEPTOR PROTEINS THAT CARRY OUT HIGH-AFFINITY BINDING AND ENERGY DEPENDENT UPTAKE INTO THE PERIPLASMIC SPACE OF SPECIFIC SUBSTRATES. IT COULD ACT TO TRANSDUCE ENERGY FROM THE CYTOPLASMIC MEMBRANE TO SPECIFIC ENERGY-REQUIRING PROCESSES IN THE CYTOPLASMIC MEMBRANE TO SPECIFIC ENERGY-RELEASE INTO THE PERIPLASM OF LIGANDS BOUND BY THESE OUTER MEMBRANE PROTEINS (BY SIMILARITY).

-i- SUBCELULUAR LOCATION: ANCHORED TO THE CYTOPLASMIC SPANS THE PERIPLASM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGRAINS; TIGRO1152; tonB Cterm; 1.
TIGRO1152; tonB Cterm; 1.
Transport; Protein transport; Inner membrane; Periplasmic; Transmembrane; Signal-anchor; Repeat; Complete proteome.
DOMAIN 1 14 CYTOPLASMIC (POTENTIAL).
TRANSMEM 15 35 SIGNAL-ANCHOR (POTENTIAL).
DOMAIN 36 280 PERIPLASMIC (POTENTIAL).
DOMAIN 36 280 PERIPLASMIC (POTENTIAL).
SEQUENCE 280 AA; 31045 MW; 640717A8BF81D76D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                         HELPY
                                                                                                                                                                                                               Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Alm R.A., Ling L.-S.L., Moir D.T.
                                                                                                                                                                            NCBI_TaxID=210;
                                                                                                                                                                                                Helicobacteraceae; Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003538; TonB.
InterPro; IPR006260; TonB_C.
Pfam; PF03544; TonB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    m R.A.,
-h D.R.,
-o P.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE TONB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; AE001549; AAD06833.1; -. F71829; F71829.
                                                                                                                                                                                                                                                   protein.
OR HP1341.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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B (Rel. 37,
l (Rel. 40,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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Last
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annotation
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Pred. No. 0.0039;
B; Mismatches
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                                                                                                                                                                                                                                                                                                                                                         285
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TRA9_MAIZE
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Best Local
Matches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986
21-JUL-1986
01-JUN-1994
                                                                       SEQUENCE FROM N.A.
MEDILINE=84205699; PubMed=6327080;
Medhan R.F., Fedoroff N.V., Messing J
The nucleotide sequence of the maize
Cell 37:635-643(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL ourse the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pylori.";
Nature 388:539-547(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE000635; AAD08383.1; -. PIR; E64687; E64687.
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                                                                                                                                                                                                                                                                                                             Spermatophyta; Magnoliophyta; Liliopsida; PACCAD clade; Panicoideae; Andropogoneae;
                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                         Putative AC9 transposase
Zea mays (Maize).
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                                                                                                                                                                                                                                                                       NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRA9_MAIZE
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MISCELLANEOUS: THIS
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SUBCELLULAR LOCATION: ANCHORED TO THE CY
MEMBRANE VIA ITS N. TERMINAL SIGNAL-LIKE
PERIPLASM (BY SIMILARITY).
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S; PR01374; TONE
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16; Conserv
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01, Last
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66.7%;
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                                               PROTEIN IS
                                                                                                                                                                                                                                                                                                             Streptophyta; Embryophyta; Tracheophyta;
yta; Liliopsida; Poales; Poaceae;
; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence up
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             BY THE
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L., Wallin
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Best Local S
Matches 23
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01-APR-1990
15-JUL-1999
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Pfam; PP02892; zf-BED; 1.
SMART; SM00614; ZnF BED; 1.
Transposable element; Transposition; DNA-binding; DNA recombination.
Transposable element; WW; 803606AA325EA042 CRC64;
     CARBOHYD
SEQUENCE
                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                     STRAIN=227(ILVALL);
MEDLINE=90067841; PubMed=2573878;
Medium E., Delius H., Carrington M., Williams R.O., R
Koenig E., Delius H., Carrington of procyclin genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRYBB
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                                                                                                       PIR;
                                                                                                                                                                                                                                                                           Nucleic Acids Res. 17:8727-8739(1989).
-!- FUNCTION: MAJOR SURFACE ANTIGEN OF PROCYCLIC FORMS.
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
-!- DEVELOPMENTAL STAGE: EXPRESSED ONLY AT A CERTAIN STAGE DURING
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                                                                                                                     EMBL;
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                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=5702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Procyclic form specific polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P14043;
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                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trypanosoma brucei brucei
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                                                                                                                                                                                                                                                               DIFFERENTIATION IN THE INSECT VECTOR.
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                                                                                                       S14896; FAUTPC.
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                                                                                       ; Antigen;
                                                                                                                   X16015; CAA34147.1; -.
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    28
94
59
115
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(Rel. 14, Last sequence update)
(Rel. 38, Last annotation update)
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                                                                                         Repeat;
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93
115
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                                                                                       Glycoprotein; GPI-anchor.
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    17 X 2 AA TANDEM REPEATS OF [DE]-P.
N-LINKED (GLCNAC. . .) (POTENTIAL).
; 6D39F0731CF0509E CRC64;
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8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             precursor
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                                                            FORM
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                                                              SPECIFIC
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Query Match
Best Local Sim
Matches 14;
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MEDLINE=9025895; PubMed=2342468;
Clayton C.E., Fueri J.P., Itzhaki J.E.,
Wisdom G.S., Vijayasarathy S., Mowatt M.
"Transcription of the procyclic acidic r
                                                                             EMBL;
                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
          Signal; Antigen; Repeat; Glycoprotein; GPI-anchor.
SIGNAL 1 27
CHAIN 28 107 PROCYCLIC FORM SPECIF
                                                EMBL; M33129; AAA30225.1; -.
EMBL; X52584; CAA36815.1; -.
PIR; A26036; A26036.
                                                                                                                                                                                                                                                                       "The procyclic acidic repetitive proteins of Trypanosoma Purification and post-translational modification."; J. Biol. Chem. 264.15088-15093(198).
                                                                                                                                                                                                                                                                                                                                                                                              Vijayasarathy S., Ernest I., Itzhaki J., Sherman D., Mowatt M.R., Michels P.A.M., Clayton C.E.; Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roditi I., Carrington M., Turner M.; "Expression of a polypeptide containing a diconfined to the insect stage of Trypanosoma Nature 325:272-274(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trypanosoma brucei brucei.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma
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16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                          STRAIN=427;
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 28-64, AND POST-TRANSLATIONAL MODIFICATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=427
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                           MEDLINE=89359323; PubMed=2475493;
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                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Attached to the membrane by a GPI DEVELOPMENTAL STAGE: EXPRESSED ONLY AT A CERTAIN STAGE
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                                                                                        X04814; CAA28503.1; -.
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xm specific polypeptide A-beta pr
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repetitive protein
                                                                                                                                                          There are no restrictions ing as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bellofatto V., R.;
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Search completed: August 26, 2003, 16:06:19 Job time: 29.0089 secs
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POBAGS;
POBAGS;
O1-AUG-1988 (Rel. 08, Created)
O1-AUG-1988 (Rel. 08, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Procyclic form specific polypeptide B1-alpha precursor (Procyclin B1-alpha) (PARP).
                                                                                                                                                                                                                                                                                       PROPEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal; Antigen; Repeat; Glycoprotein; GPI-anchor.
SIGNAL 1 27
CHAIN 28 121 PROCYCLIC FORM SPECIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M17027; AAA30222.1; -. PIR; A26918; A26918.
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NCBI_TaxID=5702;
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STRAIN=Treu 667;
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59
143 AA;
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59
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129 AA;
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107 GI
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GPI_ANCHOR.
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OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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3: sp_fungi:*
4: sp_human:*
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584
1 MRYMILGLLALAAV
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             830525 seqs, 258052604 residues
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                            sp_invertebrate:*
sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_phage:*
sp_plant:*
sp_vident:*
sp_vident:*
sp_vites:*
sp_vitebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Match Length	DB	ID	Description
ב	256.5	43.9	130	4.	Q8N2R4	Q8n2r4 homo sapien
N	247.5	42.4	755	σ	Q9BG80	Q9bg80 equus cabal
ω	245.5	42.0	817	4	014592	014592 homo sapien
4	236	40.4	755	11	Q9R0G6	
ທ	236	40.4	755	11	Q8VI54	
6	195.5	33.5	724	4	Q8N4T2	_
7	153	26.2	1319	4	094885	_
80	146.5	25.1	863	11	Q9QYS3	Q9qys3 mus musculu
9	146.5	25.1	963	11	Q9Z1T2	Q9z1t2 mus musculu
10	133	22.8	272	ഗ	Q25648	Q25648 plasmodium
11	133	22.8	332	ຫ	Q25649	Q25649 plasmodium
12	132	22.6	3164	12	880690	Q69088 human herpe
13	127	21.7	2387	16	Q8FFF8	Q8fff8 escherichia
14	126	21.6	416	ຫ	Q03752	Q03752 plasmodium
15	124	21.2	910	11	Q9JLE8	Q9jle8 mus musculu
16	124	21.2	912	11	Q9JLE7	Q9jle7 mus musculu

45	44	43	42	41	40	39	38	37	36	35	34	ω u	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
117	117	117	117	117	118	118	118	118.5	119	119	119	119	120	120	120	120	120	120.5	121	121	121	121.5	122	122	122	123	123	124
20.0	20.0	20.0		20.0	•			20.				20.	20.		20.	20.5			•	20.7	20.7	20.8	20.9	20.9	20.9	21.1	21.1	21.2
480	358	309	220	220	2344	422	165	374	667	230	164	104	377	376	374	277	273	565	704	675	378	170	400	378	259	686	823	1494
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Q27033	Q8W265	Q89402	Q8C550	Q8R2S3	8AEN6Ö	Q8X3E0	Q22168	Q8T4N5	035745	Q8SAT0	Q8LLU1	Q8V9Y2	Q9S6L9	Q54071	033899	Q27045	Q9ARY7	015754	Q9JLQ4	Q9EPT3	Q9ZNY1	Q9M5X3	Q15184	Q9LB09	Q8WV24	Q9JLE9	Q9EQF1	088902
. Q27033 theileria p	Ů,	Q89402 paramecium	Q8c550 mus musculu	Q8r2s3 mus musculu	Q9n3y8 caenorhabdi	Q8x3e0 escherichia	Q22168 caenorhabdi	Q8t4n5 glossina pa	O35745 mus musculu		Q8llu1 saccharum h	N	Q9s619 streptococc	Q54071 streptococc	O33899 streptococc	Q27045 theileria p	Q9ary7 oryza sativ	015754 dictyosteli	Q9jlq4 mus musculu	snm		Q9m5x3 oryza sativ	Q15184 homo sapien	Q9lb09 vibrio para		Q9jle9 rattus norv	Q9eqf1 rattus norv	O88902 rattus norv

ALIGNMENTS

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10 68	Submitted (WAR-2002) Submitted (WAR-2002) EMBL; AK074508; BAC11 Hypothetical protein. SEQUENCE 130 AA; 1 Submitted (WAR-2002) SEQUENCE (WAR-2002)	SEQUENCE FROM TISSUE=Embryo TISSUE=Embryo Isogai T., Ot: Suzuki Y., Na; Yamamoto J., 'I Masuho Y., On Hattori A., Ol	QBMAK4; 01-OCT-2002 (TrEMBL) 01-OCT-2002 (TrEMBL) 10-OCT-2002 (TrEMBL) Hypothetical protein Homo sapiens (Human) Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID-9606;	1 8N2R4
LIALAAVCSAAKKGSSLGGDCCSDLGPOMLRELOETNAALODVRDWLROOVREITFLKNT : ::	encing to the 031.1; 3832 M 43.9%; 56.0%; ive	III SEQUENCE FROM N.A. TISSUE-Embryo; Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K., Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N., Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;	(TrEMBLrel. 22, Cr (TrEMBLrel. 22, La (TrEMBLrel. 22, La protein FLJ90027. (Human). (Human). chordata; theria; Primates;	PRELIMINARY;
GDCCSDLGPQMLRESDLGPQMLRE 2PKPQPQPPP	EMBL/GenBank/DDBJ d W; BFE7E5EBBE7BACDD SCORe 256.5; DB 4 Pred. No. 1.6e-18; P; Mismatches 23	s T., Hayashi S., Ishii S., Nakamura Y., K , Yoshikawa Y.	eated) st sequenc st annotal Craniata; Catarrhin:	PRT; 130
SSILGGDCCSDLGPQMLRELQETNAALQDVRDWLRQ	EMBL/GenBank/DDBJ databases, -, -, -, -, -, -, -, -, -, -, -, -,	Hayashi K., Otsuki T., Ishii S., Kawai-Hio Y., Ishii S., Koyaina S., Nagal Iikawa Y., Aotsuka S., i	ed) sequence update) annotation update) aniata; Vertebrata; Eutel arrhini; Hominidae; Homo	AA.
LROOVREITFLKNT LROOVREITFLKNT IGS 103 - - RGA 114	h 130; B 17; Gaps	i T., Sugiyama T., o Y., Saito K., o Y., Saito K., Nagahari K., S., Sasaki N.,	Euteleostomi; Homo.	
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Best Local
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InterPro; IPRO0181; EGF Ca.
InterPro; IPRO02209; EGF like.
InterPro; IPRO03167; tsp_3;
Pfam; PF02412; tsp_3; 10.
SMART; SM00179; EGF CA; 2.
PROSITE; PS00118; EFF HAND; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01187; EGF CA; 2.
EGF-like domain; Matrix protein.
SEQUENCE 755 AA; 82162 MW; 170
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Q9BG80;
01-JUN-2001 (TrEMBLrel. 17, C:
01-JUN-2001 (TrEMBLrel. 17, L:
01-MAR-2003 (TrEMBLrel. 23, L:
Cartilage oligomeric matrix p:
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01-JAN-1998
01-JAN-1998
01-MAR-2003
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Gordon L., Kyle A., Ramirez M.,
Christensen M., Bruce R., Quan (
Olsen A.O., Carrano A.V.;
"Sequence analysis of an ~1 Mb)
                                                                                                    EMBL;
                                                                                                                                                               "Sequence analysis of 19p12.";
Submitted (NOV-1997)
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Dudhia J., Williams D., Smith R.K.;

Dudhia J., Williams D., Smith R.K.;

"Molecular characterization and tissue distribution of e
cartilage oligomeric protein (thrombospondin 5).";

Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF325902; AAG59881.1; -.

HSSP; P35444; 1UDF.
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Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Pe
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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                                      InterPro;
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alia; Eutheria; Perissodactyla; Equidae; Equus.
_TaxID=9796;
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P35444; 1VDF
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IPR002048; EF-hand.
IPR001881; EGF_Ca.
IPR006209; EGF_like
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                              1997) to the AAB86501.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.4%; Score 247.5; DB 6 63.2%; Pred. No. 8.7e-17; tive 11; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05,
23,
                                                                                                                                                                                                                         ~1 Mb region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                               EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence up Last annotation protein.
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                                                                                                                                                                                                                                                                                   , Adamson A.W., Bu
M., Stilwagen S.,
an G., Montgomery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17CDFA4B1A79ECE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    817
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                                                                                                                                                                                                                                                                                                                                                    Burkhart-Schultz K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
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                                                                                                                                                               databases
                                                                                                                                                                                                                                                                                       Garnes
M., Ow
                                                                                                                                                                                                                            the MEF2B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
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R EMBL;

R HSSP; P35444; ILL.

JR MGD; MGI:88469; Comp.

DR InterPro; IPR002048; EF-hand.

DR InterPro; IPR002048; EF-like.

InterPro; IPR00209; EGF_like.

DR InterPro; IPR003367; tsp_3, 9.

DR Pfam; PF02412; tsp_3, 9.

DR SMART; SM00179; EGF CA; 2.

DR PROSITE; PS00108; EF HAND; 1.

DR PROSITE; PS01186; EGF CA; 2.

DR PROSITE; PS01187; EGF CA; 2.

DR PROSITE; PS01187; EGF CA; 2.

DR PROSITE; PS01187; EGF CA; 2.

CMR EGF-like domain; Matrix protein; Signal.

EGF-Like domain; Matrix protein; CARTILAGE OLIGOMERIC MATRIX PROTEIN.

20 755 CARTILAGE OLIGOMERIC MATRIX PROTEIN.

21 19 CARTILAGE OLIGOMERIC MATRIX PROTEIN.

22 755 CARTILAGE OLIGOMERIC MATRIX PROTEIN.

23 7352 MW; 7DDFCF443589A0B7 CRC64;
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Q9R0G6
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                                                                                                                                                                                       Query Match
Best Local S
Matches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

TISSUE=Cartilage;
Fang C., Carlson C.S., Leslie M.P.,
Ni L., Di Cesare P.E.;
"Molecular Cloning, Sequencing, Tiss
Mouse Cartilage Oligomeric Matrix Pr
J. Orthop. Res. 0:0-0(1999).

EMBL; AP031530; AAD01972.1; -.
HSSP, P35444; IVDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003367; tsp_3.

Pfam; PF02412; tsp_3; 11.

SMART; SM00179; EGF CA; 2.

PROSITE; PS00018; EF HAND; 1.

PROSITE; PS01186; EGF 2; 1.

PROSITE; PS01187; EGF CA; 2.

EGF-like domain.

SEQUENCE 817 AA; 89148 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S MO
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01-MAR-2003 (TrEMBLre
Cartilage oligomeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9R0G6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 67.1 55; Conservative
                           VMECDACGPQPQPKPQPQPQPKPQP
                                                                                         VLALAILRATGQGQIPLGG----
                                                                                                                      LLALAAVCSAAKKGSSLGGDCCSDLGPQMLRELQETNAALQDVRDWLRQQVRBITFLKNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VMECDACGPQ-----PQPKP
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VMECDACGMQPARTPGLSVRPVPLCAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 13, (TrEMBLrel. 13, (TrEMBLrel. 23,
                                                                                                                                                                                       Conservative
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67.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           matrix protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leslie M.P.,
                                                                                                                                                                                  Score 236; DB
Pred. No. 1.3e
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
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6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 245.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70551980BE221855 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue
                                                                                           DLAPOMLRELQETNAALQDVRELLRHEVKEITFLKNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11;
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                                                                                                                                                                                    Gaps
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Best Local S
Matches 52
                                             Submitted (UL-2002) to the EMBL/GenBank/DDBJ dat

EMBL; BC033676; AAH33676.1; -.

InterPro; IPR002048; EF-hand.

InterPro; IPR001881; EGF_Ca.

InterPro; IPR006209; EGF_Tike.

InterPro; IPR006210; IEGF.

SMART; SM00101; EGF; 4.

SMART; SM00101; EGF; 4.

SMART; SM00101; EGF; 4.

SMART; SM00101; EGF; 4.

SMART; SM00101; EGF; 2.

PROSITE; PS001186; EGF 2; 1.

PROSITE; PS01187; EGF_CA; 2.

Matrix portain
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Pfam; PF02412; tsp_3; 9.

SMART; SM00119; EGF CA; 2.

PROSITE; PS01186; EGF 4:1.

PROSITE; PS01187; EGF CA; 2.

PROSITE; PS01187; EGF CA; 2.

EGF-like domain; Matrix protein.

SEQUENCE 755 AA; 82286 MW; 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8VI54
Q8VI54;
Q1-MAR-2002
Q1-MAR-2002
Q1-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to cartilage oligomeric matrix protein (pseudoachondroplasia, epiphyseal dysplasia 1, multiple)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8N4T2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Mouse Cartilage Oligomeric Matrix Protein Genomic Sequ
Submitted (Apr-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF257516; AALJ6518:1; -.
InterPro: IPR002048; EF-hand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
Matrix protein.
SEQUENCE 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FISSUE=Brain, and Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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IPR006209; EGF_like.
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(TremBirel. 20, Last sequence update)
(TremBirel. 23, Last annotation updat)
ligomeric matrix protein.
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Primates;
79696 MW;
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Pred. No. 1
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9AE2DB3F88815FA1 CRC64;
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. No. 1.3e-15;
ismatches 23;
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Best Local S
Matches 38
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Best Local S
Matches 41
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InterPro; IPR001660; SAM.
InterPro; IPR001452; SH3.
Pfam; PF00536; SAM; 2.
Pfam; PF00536; SAM; 1.
SMART; SM00454; SAM; 2.
SMART; SM00456; SH3; 1.
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01-MAY-1999
01-MAY-1999
                                                                                                                                                                                                                                             01-MAY-2000
01-MAY-2000
01-MAR-2003
                                                              THBS4.
Mus musculus (Mouse).
Mus musculus (Mouse).
Mus musculus (Mouse).
Metazoa; Chordata;
Metazoa; Rodentia;
                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2003 (TrEMBLrel. 23, Thrombospondin 4 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                              Q9QYS3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nagase T., Ishikawa K., Suyama M., Kikuno R., Miyajima N. Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human The complete sequences of 100 new cDNA clones from brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99087487; PubMed=9872452;
Nagase T., Ishikawa K., Suyama M.,
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-WAY-1999 (TYEMBLrel. 10, Created)
01-WAY-1999 (TYEMBLrel. 10, Last sequence)
01-WAR-2003 (TYEMBLrel. 23, Last annotati.
Hypothetical protein KIAA0790 (Fragment).
SEQUENCE FROM N.A
                                                    NCBI_TaxID=10090;
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DNA Res. 5:277-286(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1319 AA;
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Primates;
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35.5%;
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Pred.
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                                                                                     Craniata; Ver
Sciurognathi;
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No. 1.6
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                                                                                            Vertebrata;
chi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                              Ą
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                                                                                                                      Euteleostomi;
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which code
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26;
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                                                                                            Mus
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QPESULT QPESUL
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Best Local S
Matches 30
                                                                                                                               EMBL; AF102887; AAC73003.1; --
HSSP; P35444; IVDF.
MGD; MGI:1101779; Thbs4.
InterPro; IPR002048; EF-hand.
InterPro; IPR001881; EGF Ca.
InterPro; IPR006209; EGF like.
InterPro; IPR003129; TSPN.
InterPro; IPR0031367; tsp_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003367; tsp_3.
Pfam; PF002008; EGF; 1.
Pfam; PF02210; TSPN; 1.
Pfam; PF02412; tsp_3; 9.
SMART; SM00179; EGF CA; 2.
SMART; SM00210; TSPN; 1.
PROSITE; PS001018; EF HAND; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01187; EGF CA; 2.
PROSITE; PS01187; EGF CA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MSD; P35444; IVDF.
MGD; MGI:1101779; Thb84.
InterPro; IPR002048; EFF-hand.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR006209; EGF_like.
InterPro; IPR003129; TSPN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9Z1T2,
Q9Z1T2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGF-like
                                                                                                                                                                                                                                                                                                                                                                                       Newton G., Weremowicz S., Morton Copeland N.G., Lawler J.;
                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99431670; PubMed=10501972; MEDLINE=99431670; Medd=10501972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                               SMART;
                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                                       "The thrombospondin-4 gene.";
Mamm. Genome 10:1010-1016(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THBS4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thrombospondin-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Newton G., Weremowicz S
Copeland N.G., Lawler J
"The thrombospondin-4 go
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99431670; PubMed=10501972;
Newton G., Weremowicz S., Morton C.C.,
     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                         n; PF00008; EGF; 1.

n; PF02210; TSPN; 1.

n; PF02412; tep 3; 9.

T; SM00179; EGF CA; 2.

RT; SM00210; TSPN; 1.
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Genome 10:1010-1016 (1999).
AF152393; AAD32714 1;
AF152392; AAD32714.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FOSPTPNTLVPIAPPAPPTRP 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QQSEPLAATSTGDFNRQFLGQMTQLNQLLGEVKDLLRQQVKETSFLRNTIAECQACGPLS 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Оркроро---ророжроркр 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     863 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
EF_HAND; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95339 MW; 68E3EE6846728E4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.1%; Score 146.5; DB 11; 37.0%; Pred. No. 1.8e-06; 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                             Jenkins
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                                                                                                                                                                                                                                                                                                                                                                                                           N.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                             Gilbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                863;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local !
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M25445; AAA29531.1;
InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR002965; Prich_extensn.
InterPro; IPR002965; TSP1.
Pfam; PF00099; tsp 1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
PRINTS; PR01217; PRICHEXTENSN.
SMART; SM00209; TSP1; 1.
PROSITE; PS50092; TSP1; 1.
PROSITE; PS50092; TSP1; 1.
NON_TER
                                                                                                                                                                                                  01-NOV-1996
01-NOV-1996
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
PROSITE;
EGF-like
SEQUENCE
                                                                              Plasmodium berghei.
Eukaryota; Alveolata;
NCBI_TaxID=5821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=87218962; PubMed=3556207; Weber J.L., Egan J.E., Lyon J.A., Wi Maloy W.L., Hockmeyer W.T.; Thasmodium berghei: Cloning of the Exp. Parasitol. 63:295-300(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium berghei.
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
NCBI_TaxID=5821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel 01, Created)
01-NOV-1996 (TrEMBLrel 01, Last sequence up
01-MAR-2003 (TrEMBLrel 23, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q25648
                                           SEQUENCE FROM N.A.
                                                                                                                                                                        Circumsporozoite protein.
                                                                                                                                                                                                                                                                   Q25649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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MEDLINE=90158693; PubMed=2406593;
                    STRAIN=NK65
                                                                                                                                                                                                                                                                                       Q25649
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                                                                                                                                                                                                                                                                                                                                                                                                      149
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                                                                                                                                                                                                                                                                                                                                                                                                                                              76
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PS01187; EGF_CA; 2.
domain.
963 AA; 106366 MW;
                                                                                                                                                                                                                                                                                                                                                                                                  PQPQPQPQPQPQPQPRPQPQPQGGNNNNKNN 180
                                                                                                                                                                                                                                                                                                                                                                                                                           PQPQPKPQPQPQPKPQPKPEPEGTGSSEKD 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FQSPTPNTLVPIAPPAPPTRP 288
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                                                                                                                                                                                                  G (TrEMBLrel.)
G (TrEMBLrel.)
G (TrEMBLrel.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    272 AA; 29408 MW;
                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.1%;
37.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.8%;
                                                                                                            Apicomplexa;
                                                                                                                                                                                               23,
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                                                                                                                                                                                               Created)
Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 2e-(
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 146.5; DB Pred. No. 2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 1.26
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 133; DB 5; Pred. No. 1.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4FF07FA62B32A051 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B8BA83B84F489FB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wirtz R.A., Charoenvit
                                                                                                            Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    circumsporozoite protein gene.";
                                                                                                                                                                                                                                                                                       332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   272
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RESULT 13
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Best Local S
Matches 20
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McNab D., Perry L.J., Scott J.E., Taylor P.;
"The complete DNA sequence of the long unique region in herpes simplex virus type 1.",
J. Gen. Virol. 69:1531-1574(1988).

EMBL; D10879; BAA01682.1; -.
InterPro; IPR006928; Herpes teg_N.
InterPro; IPR005210; Herpes teg_N.
InterPro; IPR005210; Herpes U136.
Pfam; PF04843; Herpes U136; 1.
Pfam; PF04843; Herpes U136; 1.
SEQUENCE 3164 AA; 335817 MW; 2E3335F9525F8C71 CRC64;
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EMBL; M28887; AAA29541.1; -.
Interpro; IPR003067; Crcmsprzoite.
Interpro; IPR002965; p_rich_extensn.
Interpro; IPR002965; p_rich_extensn.
Interpro; IPR000884; TSp1.
Pfam; PF00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
PRINTS; PR01303; CRCMSPRZOITE.
PRINTS; PR01217; PRICHEXTENSN.
SMART; SM00209; TSp1; 1.
PROSITE; PS50092; TSp1; 1.
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Viruses, dsDNA viruses, no RNA stage; Herpesviridae;
Alphanerpesvirinae; Simplexvirus.
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                                       Escherichia coli 06.
Bacteria; Proteobacteria;
                                                                                                                                                     YapH homolog.
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"Sequence of the circumsporozoite
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Pred. No. 1.5e-05;
8; Mismatches 4
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Pred. No. 0.00021;
5; Mismatches 6
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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01-NOV-1996
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Colomer-Gould V., Enea V.;
Colomer-Gould V., Enea V.;
"Plasmodium yoelii nigeriensis circumsporozoite gene structure implications for the evolution of the repeat regions.";
Mol. Biochem. Parasitol. 43:51-58(1990).
EMBL; M58255; AAA29528.1; -.
InterPro; IPR003067; CCCmsprzoite.
InterPro; IPR003067; CCCmsprzoite.
Pfam; PF00090; tsp 1; 1.
Pfam; PF00090; tsp 1; 1.
Pfam; PR01303; CRCMSPRZOITE.
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                             GABA-A receptor epsilon-like GABRE OR EPSILON.
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NCBI_TaxID=5861;
                Mus musculus (Mouse)
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 Eukaryota; Metazoa;
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MEDLINE=22388234; PubMed=12471157;
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45135 MW;
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                                                                                                                                                                                                                                                                                21.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23,
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4;
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Pred. No. 0.00
4; Mismatches
                                                                                                                                                                                                                                                                                Score 126;
Pred. No. 9.
 Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                 BD8C6AD168BEB7F0 CRC64;
                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                               Length 416;
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OX MCBI_TaxID=10090;
RN (1]
RN SCQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RY MEDILINE-20266187; PubMed=10804200;
RX MEDILINE-20266187; PubMed=10804200;
RX MEDILINE-20266187; PubMed=10804200;
RT GABAR receptor epsilon and theta subunits display unusual structural
RT variation between species and are enriched in the rat locus
RT variation between species and are enriched in the rat locus
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OM protein - protein search, using sw model
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A_Geneseq_19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
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14: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
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24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
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Gapop 10.0 , Gapext 0.5
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148.232 Million cell updates/sec
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12:
13:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIE

Result No.	Score	Query Match Length DB	Length	BB	ID	Description
_	20	100.0	4.	14	AAR41971	Mammalian endoplas
N	20	100.0	4	15	AAR48246	Endoplasmic reticu
ω	20	100.0	4	15	AAR49442	Immunomodulatory t
4	20	100.0	4.	15	AAR49584	Sequence of endopl
ຫ	20	100.0	4.	17	AAR95219	Pseudomonas exotox
6	20	100.0	4.	17	AAR94944	Microsomal retenti
7	20	100.0	4.	17	AAR95063	Mammalian endoplas
8	20	100.0	4.	18	AAW31861	Endoplasmic reticu
9	20	100.0	4.	18	AAW21969	Linker #3 for immu
						•

	AAB9899	N	4.	00.	20	45
d seg	AABB	N	2.	00.	20	44
de ret	0356	N	4.	100.0	20	43
	AAE05	Ŋ	4.	8	20	42
n rete		2	4	8	20	41
98	AAG67	Ŋ	4	8	20	40
ICAM-1	AAU0719	N	4	8	20	39
ם	ABG9914	N	4	8	20	38
н	AAY323	2	4	8	20	37
O	AAY568	2	4.	8	20	36
Mammalian cytoplas	AAY6969	2	4	80.	20	35
Mammalian cytoplas	AAY904	2	4.	80.	20	34
Rat endoplasmic re	AAY7069	2	4.	80.	20	33
Endoplasmic reticu	AAY9204	2	4.	8	20	32
Protein localisat	AAY9815	2	4	80.	20	<u>3</u>
	AAY9373	2	4	00.	20	30
Endoplasmic reticu	AAB0319	2	4	00.	20	29
þ	AAB0991	2	.4	8	20	28
1 ac	AAB302	2	.4	100.0	20	27
Pseudomonas sp	AAW9291	2	4.	80.	20	26
Pseudomonas sp.	AAW92	2	4	8	20	25
Endoplasmic reticu	AAW9634	2	4	8	20	24
Endomembrane reten	AAWE	2	.4.	00.	20	23
æ	AAY2717	2	.4	100.0	20	22
2	AAY2	2	4	8	20	21
Organelle targetin	AAY3005	2	4.	00.	20	20
2	AAY2963	2	4	<u>.</u>	20	19
9	AAY4970	20	4.	8	20	18
Peptide used to mo	ABB7620	20	4	00.	20	17
	9 AAW52264	15	4	00.	20	16
C-terminal sequenc	AAW51	15	4.	00.	20	15
C-terminal sequenc	9 AAW51434	1.5	4.	8	20	14
C	9 AAW56513	15	4.	00.	20	13
Endomembrane reten	AAW615	19	4	<u>.</u>	20	12
æ	AAW646	15	4.	00.	20	11
Endoplasmic retic	9 AAW76396	15	4.	100.0	20	10

ALIGNMENTS

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RESULT 1
AAR41971
ID AAR4
XX
25-MAR-2003
10-MAR-2003
22-OCT-1993
WPI; 1993-198976/25.
                                                                                                                                                   yeast expression cassette; yeast alpha-factor leader; KE heterologous protein production; mating pheremone; YAP3; dibasic processing endoprotease.
                                                                                                                                                                                                                                               AAR41971;
                                                                                                                                                                                                                                                                AAR41971 standard; peptide; 4 AA.
                 Chaudhuri B, Riezman H,
                                                           16-DEC-1991;
                                                                             08-DEC-1992;
                                                                                               23-JUN-1993.
                                                                                                                  EP548012-A1
                                                                                                                                                                                        Mammalian endoplasmic reticulum retention signal.
                                  (CIBA ) CIBA GEIGY AG. (NOVS ) NOVARTIS AG.
                                                                                                                                    Mammalia.
                                                                                                                                                                                                         (updated)
(updated)
(first entry)
                                                            91EP-0810984
                                                                              92EP-0810964.
                 Seeboth P,
                 Stephan C;
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RESULT 2
AAR48246
ID AAR4
XX AAR4
XX AAR4
XX AAR4
XX AAR4
XX Sing
DT 25-V
DT 29-J
XX Synt
XX endc
XX endc
XX endc
XX Hop:
PD 03-F
PP 16-J
XX IN-L
PP Wit
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XX Cla
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                       New vector systems comprise a sequence adapted for intracellular delivery and expression contg. a promoter operably linked to an antibody gene encoding an antibody which binds to a specific target antigen. The antibody is esp. a single chain antibody in which the heavy and light chain variable regions are joined via a hydrophilic linker peptide. Localisation seguences are pref. included in the constructs. See AAR48246-9 and AAR48252-3 for pref. (known) endoplass reticulum retention signals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Single chain antibody; sFv; heavy chain; light chain; kappa; variable domain; hydrophilic linker; antibodies;
                                                                                                                                                                                                                                                                                Claim 32;
                                                                                                                                                                                                                                                                                                                     Intracellular binding of antigens - by using antibody targetting with vector system, for e.g. tumour suppression
                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haseltine WA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-FEB-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-JUL-1992;
17-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-JUL-1993;
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29-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR48246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR48246 standard; peptide; 4 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (DAND ) DANA
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(first entry)
                                                                                                                                                                                                                                                                              99; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Marasco
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93US-0045274.
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Pred. No. 9.3
D; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INC
                     PN field.)
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hes 0;
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RESULT 3
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                                                        Query Match
Best Local
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Best Local
                                                                                                                                                                                                                                                                                                                                                               Chicz RM,
Vignali DA;
                                                                                                               reduce transplant rejection. They may also be used f providing an exclusively T-cell-mediated response, wh class I or class-II based, or both, depending on the character of the immunogenic peptides.

(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                       The sequences given in AAR49291-505 and AAR46981-7038 represent pept fragments of naturally-occuring immunomodulatory proteins. These fragments are between 10-30 residues in length and bind to a human major histocompatibility complex (MHC) classified allotype. These peptides may be used for therapy of autoimmune diseases, such as type I diabetes, rheumatoid arthritis and mutiple sclerosis, and to reduce transplant rejection. They may also be used for vaccination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Naturally-occuring; immunomodulatory protein; human; therapy; class I; major histocompatibility complex; class II; allotype; type I diabetes; autoimmune disease; rheumatoid arthritis; T-cell-mediated response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                           Sequence
                                                                                                                                                                                                                                                                                                       Novel immunomodulatory peptide(s) and nucleic acids - useful for treatment of auto:immune diseases, transplant rejection and for
                                                                                                                                                                                                                                                                                                                                                                                                                          11-AUG-1992;
15-JUN-1993;
                                                                                                                                                                                                                                                                     Claim 13; Page 94; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-MAR-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mutiple sclerosis; transplant rejection; vaccine; MHC
                                                                                                                                                                                                                                                                                                                                          WPI; 1994-082825/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-AUG-1993;
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16-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR49442 standard;
                                                                                                                                                                                                                                                                                                                                                                                                    (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9404171-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunomodulatory trafficing sequence
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                                           Similarity 4; Conserv
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                   KDEL
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                                                                                           4 AA;
                                                                                                                                                                                                                                                                                                                                                                           Hedley ML,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
                                             Conservative
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                          92US-0925460.
93US-0077255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             93WO-US07545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                        100.0%;
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                                                        Score 20;
Pred. No.
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Pred. No.
                                              Mismatches
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                                                     9.3e+05;
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                                                                     В
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                                                                   Length 4;
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                                                                                                                                                                                                                                                                                                                                                                             Urban
                                             Indels
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                                             Gaps
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ARPSULT 5
AAR95219
ID AAR9
XX AAR9
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XX AAR9
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XX Anti
KW diag
XW immu
XX immu
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AAR49584
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Best Local (
                                                                                                                                                                                                                                                                                                                                         A trafficking sequence is an AA sequence which functions to control intracellular trafficking (directed movement from organelle to organelle to the cell surface) of a polypeptide to which it is attached. Such trafficking sequences might traffic the polypeptide to ER, a lysosome, or an endosome, and include signal peptides, ER retention peptides such as AAR49584; and lysosome-targeting peptides such as AAR49585 and AAR49587 and lysosome-targeting peptides such as AAR49585 and AAR49587 and lysosome-targeting peptide with such a function is the signal peptide of MHC class II alpha (AAR49587). (Updated on 25-MAR-2003 to correct PN field.)
            Antibody; fusion protein; single chain; inhibition; tumour; diagnosis; detection; imaging; immunotoxin; targetting; assay; immunoassay; Lewis(Y) carbohydrate antigen.
                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; Page 49; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New peptide binding to MHC class II allotype - useful for treating auto-immune diseases, transplant rejection and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
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15-SEP-1994
                                                                Pseudomonas
                                                                                          16-DEC-1996
                                                                                                                     AAR95219;
                                                                                                                                           AAR95219 standard; protein; 4 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1994-083102/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chicz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ımmunisation
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`i DAA;
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                                                                                                                                                                                                                                                                                                                   4 AA;
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                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             endoplasmic reticulum (ER) retention peptide
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                                                                                         (first entry)
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92WO-US06692
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                                                                                                                                                                                                                                                                            100.0%;
                                                                modified C-terminal
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Pred. No. 9.3e+05;
                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strominger JL,
                                                               sequence.
                                                                                                                                                                                                                                                                                       Length
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Best Local :
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28-OCT-1994;
28-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          heavy chains of an antibody (Ab) fused together, and an effector molecule, where the fusion protein or Ab has the binding specificity of monoclonal Ab (MAb) B1, B3 or B5, can be used for the production of such fusion proteins or antibodies. The fusion proteins can be used in compositions as an immunotoxin to inhibit tumour cell growth. The single chain antibody can be used to detect the presence or absence of cells bearing a Lewis(Y) carbohydrate antigen in a patient. The antibodies are also useful as multiple targetting moieties, providing at least 2 kinds of biological activity. They can also be used in diagnostic assays and for the imaging of tumours when attached to a radiolabel and for the pathological diagnostic functions.
                                                                                                                                                                                                                                                                                                                                                                                          various amino acid deletions in domains II and III, single amino acid substitutions and addition of one or more sequences at the C-terminal end. The wild type C-terminal sequence of the Pseudomonas exotoxin is given in AAR95221.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumours. Humanised antibodies are less immunogenic than the mouse MAbs B1, B3 and B5, making them more suitable for long term treatment. The effector molecule used is preferably a drug or cytotoxin which then produces an immunotoxin capable of selectively killing particular cells. Preferred toxins are the Pseudomonas exotoxin or Diphtheria toxin. These are both highly toxic compounds and so are modified to eliminate domain Ia of the Pseudomonas toxin,
                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Single chain fusion proteins and antibodies - useful to diagnose treat cancer, specifically bind Lewis(Y) related carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Benhar I,
Padlan EA,
                                            Microsomal retention signal.
                                                                                                                                              AAR94944 standard; Protein; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A novel recombinant DNA molecule which encodes a single chain fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 14; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-MAY-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                             l Similarity
4; Conserv
                                                                                                                                                                                                                                                         1 KDEL 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or antibody comprising the Fv region of both the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brinkmann U, F
Pai L, Pastan
                                                                                                                                                                                                                                                                                                                                                                4 AA;
                                                                                                                                                                                                                                                                                                 Conservative
                                                                             (first entry)
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94US-0331396.
94US-0331397.
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                                                                                                                                                                                                                                                                                             100.0%; Score 20; Di
100.0%; Pred. No. 9.:
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                             ; DB 17;
. 9.3e+05;
ches 0;
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am M;
                                                                                                                                                                                                                                                                                                                              Length 4;
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Toxin; subunit; vaccine; transgenic plant; immunogen; antigen; adjuvant; immunisation.

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RESULT 7
AAR95063
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Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A transgenic plant comprising or expressing a DNA sequence encoding an immunogenic agent can be be used as an oral vaccine for animals. The vaccine is administered by the oral consumption of the plant and provides the first known functional method for immunising animals using transgenic plants, where the plants express bacterial antigens that act as both immunogens and adjuvants. The method provides an inexpensive production and delivery system for such antigens to animals. This sequence acts as a microsomal retention signal and was used to modify the LT-B Escherichia coli toxin subunit C-terminal sequence. The sequence coding for the whole LT-B gene was used in the construction of such a transgenic plant. The immunogenic agent preferably comprises the LT-B or CT-B (cholera toxin B subunit) or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                        01-NOV-1994;
                                                                              09-MAY-1996
                                                                                                      WO9613599-A1
                                                                                                                               Synthetic
                                                                                                                                                         endoplasmic reticulum.
                                                                                                                                                                                  Nucleic acid transfer system;
                                                                                                                                                                                                            Mammalian endoplasmic reticulum retention signal.
                                                                                                                                                                                                                                                                 AAR95063;
                                                                                                                                                                                                                                                                                        AAR95063 standard; Peptide; 4 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         optionally LT-A or CT-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 13; Page 95; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transgenic plants contg. E. coli heat laused as oral vaccines for animals which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arntzen CJ,
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(WELS/) WELS
                                                  31-OCT-1995;
                                                                                                                                                                                                                                       22-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TULA ) TULANE EDUCATIONAL FUND (TEXA ) UNIV TEXAS A & M SYSTEM
                                                                                                                                                                     targeting; multidomain
                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
4; Conserv
                                                                                                                                                                                                                                                                                                                                                                          KDEL 4
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A;
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ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                      (first entry)
                           94EP-0810627
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                                                    95WO-EP04270
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                                                                                                                                                                     n; gene transfer; gene therapy;
protein; vector; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coli heat labile enterotoxin subunits
                                                                                                                                                                                                                                                                                                                                                                                                        Score 20; DB 1/;
Pred. No. 9.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mason HS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    consume the plant
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 4;
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RESULT 8
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Best Local
This sequence represents a endoplasmic reticulum retention peptide, and can be used in the method of the invention. The method is for producing an RNA-loaded antigen presenting cell (APC) that presents on its surface a tumour or pathogen antigenic epitope (TAE or PAE respectively) that induces T cell proliferation and an immune response against the tumour or
                                                                                                                                                                                                                                                                                                                                                                                                 RNA-loaded antigen presenting cell; trafficking sequence; APC production; tumour formation; pathogen infection; antigenic epitope; immune response; T cell proliferation; cytotoxic T lymphocyte; adoptive immunotherapy; therapy; TAE; CTL; PAE; endoplasmic reticulum retention peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Endoplasmic reticulum retention signals include a mammalian signal (AAR95063), a bacterial signal (AAR95064) from Pseudomonas exotoxin, and a yeast signal (AAR95065). The signal may form part of a multidomain protein (see also AAR95053-58) that is used with an effector nucleic acid for the transfer of nucleic acids to targeted cells as a means of gene therapy. The endoplasmic reticulum retention signal functions to affect intracellular routing of the internalized protein/nucleic acid complex.
                                                                                                                             Use of RNA-loaded antigen presenting cells - to induce T-cell proliferation for the treatment or prevention of tumour forma
                                                                                                                                                                                                                                                                                      30-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid transfer system for gene therapy, e.g. against cancer - includes toxin translocation domain to target nucleic acid to
                                                                                     Claim 49;
                                                                                                                                                                         WPI; 1997-549715/50
                                                                                                                                                                                                                                                          30-APR-1996;
                                                                                                                                                                                                                                                                                                                    06-NOV-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW31861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW31861 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                  Boczkowski DJ,
                                                                                                                                                                                                                                (UYDU-) UNIV DUKE
                                                                                                                                                                                                                                                                                                                                              WO9741210-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 11; 106pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
4; Conserv
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                                                                                     Page 38; 47pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       reticulum retention peptide
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                                                                                     English.
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Pred. No. 9.3
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Best Local :
AAW21967-W21969 represent linkers used in the immunotoxins of the invention. The immunotoxins bind to target cells, and comprise, a Besudomonas exotoxin (PB) that does not need proteolytic activation for cytotoxic activity fused to a VH framework region of an Fv antibody (Ab) fragment. The VH chain region is bound through at least one disulphide bond to a variable light (VL) chain framework region. The PE is lacking residues 1-279 and is at least 10-fold more cytotoxic to the target cells than an immunotoxin comprising PE attached to a VH chain framework region of an Fv Ab fragment lacking a disulphide bond to a VL chain framework region. These sequences are used to join the VH chain region the PE. The immunotoxins can be used for killing target cells in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCR; primer; amplify; polymerase chain reaction; antibody; immunotoxin; variable heavy chain; VH; murine monoclonal antibody; Lewisy; carcinoma; carbohydrate antigen; Pseudomonas exotoxin; proteolytic activation; cytotoxic activity; tumour; autoimmune condition; rheumatoid arthritis; graft versus host disease; organ transplant rejection; type I diabetes; multiple sclerosis; systemic lupus erythematosus; myasthenia gravis; multiple sclerosis; systemic lupus erythematosus; myasthenia gravis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pathogen, and comprises introducing into an APC in vitro, RNA that encodes the antigen. The RNA-loaded APCs can be used to stimulate cytotoxic T lymphocyte (CTL) proliferation ex vivo or in vivo. The ex vivo expanded CTL can be administered to a patient in a method of adoptive immunotherapy. The methods can be used for treating or preventing tumour formation or pathogen infection caused by e.g. HIV, hepatitis, influenza, poliomyelitis, measles, herpes, mumps or rubella viruses, Salmonella, Shigella or Enterobacter. The method circumvents tneed to purify RNA or isolate and identify a TAE or PAE.
                                                                                                                                                                                                                                                                          Immuno:toxin(s) comprising Pseudomonas exotoxin linked to di:sulphide stabilised variable heavy and light chain regions of antibody - useful for killing target cells bearing characteristic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR; primer; amplify; variable heavy chain;
                                                                                                                                                                                                                              Claim 9;
                                                                                                                                                                                                                                                                     marker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Linker #3 for immunotoxin containing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 AA;
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                                                                                                                                                                                                                            50; 64pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytosol; bone marrow;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transplant; therapy.
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cheв 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treatment of tumours, autoimmune conditions, graft versus host disease, organ transplant rejection, type I diabetes, multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus, myasthenia gravis, etc, all caused by T and B cells. They can also be used to deliver an antibody to the cytosol of a cell, and in vitro in the elimination of harmful cells from bone marrow before transplant. The immunotoxins have high cytotoxicity to target cells and a small size to provide greater penetration to target cells.
                                                                       in the intracellular transport and cytotoxicity of ETA. This suggests that ETA interacts with the KDEL receptor and that ETA may reach the interior of the EF before penetrating the cytosol. The invention provides a means of delivering compounds to cells as conjugates with modified ETA. The modified ETA is able to cross
                                                                                                                                                 for returning back to the endoplasmic reticulum (ER) proteins that have escaped the ER and entered to Golgi complex. The mechanism involves the KDEL receptor. The KDEL motif can replace a REDL motif (see AAW76395) present at the C-terminal end of Pseudomonas aeruginosa exotoxin A (ETA, see AAW76391). This motif is important
                                                                                                                                                                                                                                                                                               Delivering compounds to cells as new conjugate with detoxified exotoxin A - able to cross membranes and deliver to the cytople.g. nucleic acids, antibodies, tumour suppressors etc.
                           chain antibodies and tumour suppressors.
                                          membranes and deliver e.g. therapeutic agents to such as nucleic acids, peptides, peptide nucleic
                                                                                                                                                                                                                                   This peptide is the consensus intracellular transport signal used
                                                                                                                                                                                                                                                                  Disclosure; Page 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ETA; drug delivery; membrane transport;
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Pred. No.
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Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents an endomembrane retention signal which is used in a method involving the construction of a target molecule from human J chain protein fragments. This construct is used in a method to target imaging agents to epithelial surfaces at which they may remain or undergo transepithelial transport via transcytosis. At least one imaging agent is linked to the targeting molecule comprising a polypeptide that (a) forms a closed covalent loop, (b) contains at least 3, preferably 4, peptide domains having beta-sheet character separated by domains lacking beta-sheet character and (c) is not full length dimeric IgA. The imaging agents are useful in the diagnosis of disease. The target molecule is also capable of specifically binding to a basolateral factor associated with an epithelial surface to cause internalisation of a biological agent linked to the target molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1c; Page 90; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New epithelial tissue targeting agent - used to deliver imaging agents to an epithelial surface for internalisation; useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9830591-A1
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AAW61591;
                                                      AAW61591 standard; Peptide; 4 AA
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tosis; disease;
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Pred. No. 9.3e+05;
; Mismatches 0;
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; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide
                                                                                                                                                                                                                                                                                                                                                          Length 4;
                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                      0
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RESULT 13
AAW56513
ID AAW56513
AC AAW56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                Intracellular targeting sequence; endoplasmic reticulum DNA vaccine; genetic immunisation; allergy; autoimmune cancer; infection; psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The endomembrane retention signal is used in the synthesis of a targeting molecule (TM). The TMs are used to target biological agents to epithelial surfaces at which they can be internalised. The TMs comprise a polypeptide that: (a) forms a closed covalent loop; (b) contains at least 3, preferably 4, peptide domains having beta-sheet character separated by domains lacking beta-sheet character; and (c) is not full length dimeric IgA. The TMs are useful to prevent and/or treat diseases associated with epithelial surfaces, e.g. asthma, cancer, (myco) bacterial, viral or fungal infection, inflammatory disorders, autoimmune disorders, celiac disease, colitis, pneumonia and cystic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J chain; targeting molecule; epithelial; beta-sheet; asthma; cancer; inflammatory disorder; autoimmune disorder; celiac disease; colitis; pneumonia; cystic fibrosis.
                                                          WO9817323-A1
                                                                                                                                                                                                                                                                               Endoplasmic reticulum recycling peptide.
                                                                                                                                                                                                                                                                                                                                          28-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW56513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New epithelial tissue targeting agent - used to deliver biologically active compounds to an epithelial surface internalisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 48; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Endomembrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fitchen JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9830592-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (EPIC-) EPICYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KDEL 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KOEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; Peptide; 4 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hein MB,
                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        retention signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0782481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-US00542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 19;
                                                                                                                                                                                                                              reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                   disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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RESULT 14
AAW51434
문
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This peptide, when joined to the C-terminus of a protein, acts as an endoplasmic reticulum (ER) recycling signal that localises the protein from the Golgi body back to the ER when expressed in a C cell. A claimed novel plasmid comprises a sequence, linked to that includes, or is linked to, an intracellular target protein C that includes, or is linked to, an intracellular targeting sequence (ITS) such as this peptide. Other ITS peptides (see AAW56512 and C AAW56514) are provided that direct localisation in the lysosome or C the ER. The novel plasmid is used as a protective or the ER. The novel plasmid is used as a protective or therapeutic DNA vaccine to immunise against the immunogenic target protein (claimed), particularly in cases of allergy, cancer (or other proliferative diseases such as gooriasis), microbial cinfection or autoimmune disease, e.g. rheumatoid arthritis, C infection or autoimmune disease, e.g. rheumatoid arthritis, C pernicious anaemia and many others. A particular use is against C pathogens that, at least for part of their life cycle, are c intracellular, e.g. hepartitis C, HIV, Neisseria gonorrhoeae, the process of the ER.

CC Listeria and Shigella. The cyctotxic T cell response is enhanced contacts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                              nuclear localisation; fluores amylopectin; mannan; inulin;
                                                                                                                                                                                                                                             C-terminal
                                                                                                                                                                                                                                                                          02-SEP-1998
                                                                                                                                                                                                                                                                                                        AAW51434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 7; Page 62; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid encoding immunogenic target protein - used in, e.g. protective or therapeutic vaccines against allergy, cancer,
              23-JUN-1993;
                                                                        30-JUN-1998
                                                                                                      US5773227-A
                                                                                                                                     Synthetic
                                                                                                                                                                 endoplasmic
                                                                                                                                                                                                                Bifunctional
                                                                                                                                                                                                                                                                                                                                      AAW51434 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               microbial infection or autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-261198/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Madaio M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-OCT-1997;
                                         23-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYPE-) UNIV PENNSYLVANIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4
                                                                                                                                                                                                                                                                                                                                                                                                                                                KDEL 4
                                                                                                                                                                                                                                        sequence of localisation peptides for the ER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Weiner DB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 AA;
                                                                                                                                                                   reticulum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                              chelating polysaccharide; targeting peptide; heparin; lisation; fluorescent indicator; dextran; ficol; glycogen; mannan; inulin; starch; agarose; cellulose; ER;
                                                                                                                                                                                                                                                                          (first entry)
            93US-0082269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97WO-US19545
                                           93US-0082269
                                                                                                                                                                                                                                                                                                                                     peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Sc.
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 9.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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RESULT 15
AAW51437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local (
                                                                                                                                         27-MAY-1992;
24-OCT-1989;
10-MAR-1994;
30-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chelating moiety selective for a monovalent or divalent metal ion (to act as a fluorescent indicator for the metal ion) and (b) at least one targeting peptide (to localise the compound to the inside of a cellular organelle). Preferably the polysaccharide is dextran, ficol, heparin, glycogen, amylopectin, mannan, inulin, starch, agarose or cellulose with a molecular weight less than 3,000,000. The metal ion is preferably Na+, K+, Li+, Ca2+ or Mg2+. The compounds are useful for analysing intracellular ion levels, especially Ca2+. The present sequence represents a carboxyl terminal sequence commonly shared by localisation peptides
                                                                                                                                                                                                                                                                                                               Endoplasmic reticulum; carboxy terminus; Golgi apparatus; glycosyltransferase; membrane anchor; oligosaccharide syn
                                                                                                                                                                                                                                                                                                                                                      C-terminal sequence of endoplasmic reticulum retained proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bifunctional chelating polysaccharides used for analysing intracellular ion levels - have chelating moieties attached which act as a fluorescent indicator in the presence of selected metal
                                                  WPI; 1998-398046/34.
                                                                                                                                                                                                           30-JAN-1996;
                                                                                                                                                                                                                                   07-JUL-1998
                                                                                                                                                                                                                                                             US5776772-A
                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                 02-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                           AAW51437;
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW51437 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a water soluble polysaccharide with a molecular weight greater than 1000 Daltons covalently attached to (a) at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Column 9; 29pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Allbritton NL,
                                                                                         Adler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for the endoplasmic reticulum (ER).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MOLE-) MOLECULAR PROBES
                                                                                                                 (REGC ) UNIV
                                                                                        ₽,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KDEL 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 100 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KDEL 4
                                                                            Browne JK,
J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 AA;
                                                                                                                 CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                               (first
                                                                                                                                        92US-0849045.
89US-0426577.
94US-0209604.
96US-0593865.
                                                                                                                                                                                                           96US-0593865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kuhn MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide; 4
                                                                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                        Colley KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Meyer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 20; DB Pred. No. 9.3 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                        Paulson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 19;
                                                                                        JG,
                                                                                        Ujita-lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 4;
                                                                                                                                                                                                                                                                                                                 synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>.</u>
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0

Expression cassette for producing glycosyltransferase in secretable form - lacking membrane anchor and Golgi retention signal, used for synthesis of oligosaccharide(s)

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XX

XX

The invention relates to expression cassettes which contain a promoter CC and a DNA sequence encoding a secreted glycosyltransferase that lacks CC the membrane anchor and the Golgi retention signal. The glycosylcransferases are used in enzymatic oligosaccharide synthesis.

CC They are produced in a soluble form that is secreted into the culture medium without loss of enzymatic activity, resulting in increased compoduction and simpler recovery (free of any membrane-bound glycosylcransferase), compared with extraction from mammalian tissue. The present sequence represents a carrboxy-terminal sequence sufficient for XX

XX

XX

Sequence 4 AA;

Query Match

Best Local Similarity 100.0%; Score 20; DB 19; Length 4;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 1 XDEL 4

Db 1 XDEL 4

Search completed: August 26, 2003, 16:04:29

Search completed: August 26, 2003, 16:04:29

Job time: 11.2832 secs
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Result
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Maximum DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                           No.
       Pred. No. score grea and is der
                                                                                                                                                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                          No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
    length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-696-872-37
20
1 KDEL 4
                                                                                                                                                                                                                                                                                                                                                                                          Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             August 26, 2003, 16:05:48; Search time 1.41593 Seconds (without alignments)
119.528 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 ,
                 100.00
100.00
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                                                                                                                                                                                                                                                                                                                                     100.0
                                                                                                                                                                                                                                                                                                                                                                100.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
                                                                                                                                                                                                                                                                                                                                                                                          Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gapext 0.5
                                         US-08-328-961-6
US-07-872-6738-5
US-07-872-6738-5
US-08-405-615-16
US-08-405-1397-6
US-08-462-397-6
US-08-462-299-7
US-08-461-234-16
US-08-461-234-16
US-08-461-234-16
US-08-461-234-16
US-08-480-190-152
US-08-480-190-152
US-08-480-190-152
US-08-480-190-152
US-08-480-190-152
US-08-480-190-152
US-08-413-190-15
US-08-413-2088-15
US-08-413-2088-15
US-08-413-2088-15
US-08-413-2088-15
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US-08-413-2088-15
US-08-413-2088-15
US-08-413-208-15
US-08-413-2088-15
                                                                                                           IS-08-461-234-16

IS-08-480-190-152

IS-08-545-151-28

IS-08-373-190-17

IS-08-463-480-16

IS-08-470-5668-51

IS-08-488-379-152

IS-08-488-379-152

IS-08-1821-840-1908-6

IS-08-193-928-15
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16, Appl
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	ALIGNMENTS	US-08-818-252-49	US-09-191-852-1	US-09-169-425C-23	US-09-169-015-38	US-09-124-671-37	US-09-215-035-7	US-08-789-333F-28	US-09-172-063-37	US-09-094-359-17	US-09-047-148-12	US-08-776-271-7	US-09-397-951-9	US-09-287-145A-17	US-08-782-480-44	US-08-718-904-42	US-08-722-258-62	US-08-350-215-17	US-08-818-253-49	
		Sequence 49, Appl	Sequence 1, Appli	Sequence 23, Appl	Sequence 38, Appl	Sequence 37, Appl	Sequence 7, Appli	Sequence 28, Appl	Sequence 37, Appl	•	Sequence 12, Appl	Sequence 7, Appli	Sequence 9, Appli	Sequence 17, Appl	•	Sequence 42, Appl	Sequence 62, Appl	Sequence 17, Appl	Sequence 49, Appl	

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US-08-328-961-6
US-08-328-961-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application Patent No. 5501975 GENERAL INFORMATION:
                                                                                                                                                              TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
RAPPLICATION UMMER: US/07/
APPLING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,94
                                                                                                                                                                                                                           REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 4-:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,961
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING XYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Seeboth, Peter
APPLICANT: Reizman, Howard
TITLE OF INVENTION: No. 5501975el DNA Molecules
NUMBER OF SEQUENCES: 15
                                                                          MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                             LENGTH: 4 amino acids TYPE: amino acid TOPOLOGY: linear
                     OTHER INFORMATION:
                                     NAME/KEY: Domain
LOCATION: 1..4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hawthorne
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Seeboth,
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                 retention signal
                     KDEL"
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Query Match

100.0%;

Score 20;

DB 1;

Length 4;

APPLICANT:

Pastan, Ira

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RESULT 3
US-08-405-615-16
i Sequence 16, Application US/08405615
; Patent No. 5602095
; GENERAL INFORMATION:
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US-07-872-673B-5
                                                                                                                                                                                                                                                                               US-07-872-673B-5
                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS: Edman, Jeffrey C., Ellis, Leland, Blacher, Russell W., Roth, Richa TITLE: Sequence of protein disulphide isomerase and implications of its rel Patent No. 5578466
                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 4; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: Japanese Patent Application No. 5578466. 114074/91 and 31160
FILING DATE: 18-APR-1991 and 30-OCT-1991
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION: APPLICANT: Toshiy
                                                                                                                                                                                                                                                                                                                                                                                                                                     IDENTIFICATION METHOD: ER retension of proteins having this signal OTHER INFORMATION: located at the C-terminus of rat PDI PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: Apple Macintosh SE
OPERATING SYSTEM: Apple DOS
SOFTWARE: Microsoft Word Version 4.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Type 2D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                      VOLUME: 317
                                                                                                                                                                                                                                                                                          PAGES: 267-270
DATE: 19-Sep-1985
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: UFILING DATE: 19920417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: ER retension signal
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                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                       4; Conservative
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C-terminal fragment
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Pred. No. 2.5e+05;
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Protein Disulfide Isomerase Gene an
                                                                                                                                                                                                                                      Length 4;
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US-08-331-398A-51
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                                                                                                                                                                                                                                                                                                                                                                     Patent No. 5608039
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-543-5043 INFORMATION FOR SEQ ID NO:
ZIP: 9410711.7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                        APPLICANT: Pai, Lee
TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
TITLE OF INVENTION: and Their Uses (as amended)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
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PRIOR APPLICATION NUMBER: 1
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ADDRESSEE: Ellen L. Weber
STREET: One Market Plaza,
                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                          APPLICANT: Willingham, Mark APPLICANT: FitzGerald, David APPLICANT: Brinkmann, Ulrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: FitzGerald, David J.
TITLE OF INVENTION: Recombinant Pseudomonas Exotoxin with
TITLE OF INVENTION: Increased Activity
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                 CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPACTIVE OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: One Market | CITY: San Francisco
                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: peptide
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                                                                                                    USA
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Pred. No. 2.5e+05;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 4;
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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INFORMATION FOR SEQ ID NO:
                             CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/989,260

FILING DATE: 11-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: Spruill, W. Murray

REGISTRATION NUMBER: 32,943

REFERENCE/DOCKET NUMBER: 4-18885/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
PILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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TELECOMMUNICATION INFORMATION: 1919-541-8614
                                                                                                                                                                               APPLICATION NUMBER: US/08/462,397
FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100
les 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0 FILING DATE: 28-OCT-1994
                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/596,289 FILING DATE: 12-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6, Application US/08462397
5. 5618690
                                                                                                                                                                                                                                                                                                                                        10532
                                                                                                                                                                                                                                                                                                                                                                                         Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T: Reizman, Howard INVENTION: No. 5618690el DNA Molecules and Hosts
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                                                                                                                                                                                                                                                                                                                                                                           Ϋ́N
                                                                                                                                                                                                                                                                                                                                                                                                            7 Skyline Drive
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                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stephan, Christine
Seeboth, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chaudhuri,
                                                                                                                                                                                                                                                                                                                                                                                                                                Ciba-Geigy Corporation
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Query Match
Best Local Similarity
Thes 4; Conserve
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                                                                                                                      TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino **'
TYPE
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SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: 'amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 89 16806.6
FILING DATE: 22-UTL-1889
APPLICATION NUMBER: PCT/GB90/01131
FILING DATE: 23-UTL-1990
APPLICATION NUMBER: US 07/820,867
FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION: .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION: APPLICANT: CAMPBE
                                                                                                                                                                                                                    REGISTRATION NUMBER: 32,925
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/270,314
                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Domain LOCATION: 1.4 OTHER INFORMATION:
                                                                                                      TOPOLOGY:
                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                        NAME: PATCH, Andrew REGISTRATION NUMBER:
                                                                                                                                                                                         TELEFAX:
                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U
ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Arlington
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                                                                                                                                                                                           (703) 521-22
(703) 685-0573
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               Conservative
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                                                                                                                                                                                                                                                    Andrew J
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Pred. No.
                            Score 20; DB 1; 1
Pred. No. 2.5e+05;
                 Mismatches
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                                           Length 4;
               Indels
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               0;
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               Gaps
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US-08-082-269D-7
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US-08-406-192-28
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CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/224,831

FILING DATE: 08-APR-1994

ATTORNEY/AGENT INFORMATION:
NAME: REDIZONI, George E
REGISTRATION NUMBER: 37,919

REFERENCE/DOCKET NUMBER: RECL18947

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 18000MAN 10000MAN 100000MAN 10000MAN 10000MAN 10000MAN 10000MAN 100000MAN 10000MAN 10000MAN 10000MAN 10000MAN 10000MAN 10000MAN 10000MAN 10000MAN 1000
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TELEX: 4938023
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                               sequence 7, Application US/08082269D Patent No. 5773227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 28, Application US/08406192 Patent No. 5739287
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Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Kuhn, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Wilbur, D. Scott
APPLICANT: Prathare, Pradip M
TITLE OF INVENTION: Bictinylated Cobalamins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
ZIP: WA 98101-2333
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                   APPLICANT: Kuhn, Michael
APPLICANT: Meyer, Tobias
APPLICANT: Meyer, Tobias
TITLE OF INVENTION: Bifunctional Chelating Polysaccharides
NUMBER OF SEQUENCES: 9
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                               CORRESPONDENCE ADDRESS:
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TOPOLOGY: lir
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FILING DATE: 16-MAR-1995
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                                                                                                                ADDRESSEE:
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Oregon
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                                                                             4849 Pitchford Avenue
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                                                                                                            Molecular Probes, Inc
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100.0%; Pred. No. 2.5e+05;
Live 0; Mismatches 0;
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US-08-593-865-1
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 AMINO ACIDS
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08593865 Patent No. 5776772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/593,865
                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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AUTHORS: Munro, Sean and Pelham Hugh, R.B.
TITLE: A C-Terminal Signal Prevents Secretion of Luminal ER Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Helfenstein, Allegra J.
REGISTRATION NUMBER: 34,179
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503)465-8300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/082,269D
FILING DATE: 23-Unne-1993
CLASSIFICATION: 435
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                        APPLICANT: Weinstein, Jasminder
TITLE OF INVENTION: Method for Producting Secretable
TITLE OF INVENTION: Glycosyltransferases and Other Golgi Processing Enzymes
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                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISSUE: 13 March 1987
PAGES: 899-907
DATE: 1987
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SOFTWARE: Text EC
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                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                  90067
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                                                                                                                                                                                                      Los Angeles
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2029 Century Park East, 38th Floor
                                                                                                                                                                 USA
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Colley, Karen J.
Adler, Beverly
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                                                                                                                                                                                                                                                                                                                                                                                                                             Paulson, James C.
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January 30, 1996
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ATTORNEY/AGENT INFORMATION:

APPLICATION NUMBER: WO 9 FILING DATE: 16 May 1991

WO 91/06635

PRIOR APPLICATION DATA:

CLASSIFICATION:

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APPLICATION NUMBER: US 08/405,615
FILING DATE: 15-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15280-36-3
TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 543-960
TELEPAX: (415) 543-960
TELEPAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-593-865-1
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Patent No. 5821238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Ve. CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,234
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/901,709
FILING DATE: 18-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (310) 277-1297 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Oldenkamp, David J.
REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 117-033
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Pastan, Ira H.
APPLICANT: FitzGerald, David J.
TITLE OF INVENTION: Recombinant Pseudomonas Exotoxin with
TITLE OF INVENTION: Increased Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: One Market
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 100.0%; Score 20; DB 1; I Local Similarity 100.0%; Pred. No. 2.5e+05; les 4; Conservative 0; Mismatches 0;
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ENGTH:
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4 amino acids
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HYPOTHETICAL: NO US-08-461-234-16
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                                                                                                            US-08-480-190-152
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                                                       Matches
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                                                                      Best
                                                                               Query Match
                                                                                                                                                                                                                                         FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
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                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM 55" Model 50Z or 55SX
OPERATING SYSTEM: WS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: June 15
APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                     TELEFAX: 200154
                                                                                                                                                                                                                  TELEPHONE: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity hes 4; Conserv
                                                                     Local
                                                                                                                                         STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                                                      Similarity 4; Conserv
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KUEL
                         KDEL 4
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                                                       Conservative
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Lawrence J. Stern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Roman M. Chicz
Dario A. A. Vignali
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                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fish & Richardson
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                                                                   100.0%;
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5, 1993
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                                                    Score 20; DB 2; L
Pred. No. 2.5e+05;
                                                                               Length 4;
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DIKE, BRONSTEIN, ROBERTS & CUSHMAN

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US-08-373-190-17
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; MOLECULE TYPE:
US-08-545-151-28
                                                                                                                                                                Sequence 17, Application US/08373190 Patent No. 5851829 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 4938023
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Morgan Jr
APPLICANT: Wilbur, D
APPLICANT: Prathare,
TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
                             APPLICANT: MARASCO, WAYNE
APPLICANT: HASELTINE, WILLIAM
TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF PROTEINS
NUMBER OF SEQUENCES: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: RETELECOMMUNICATION INFORMATION: TELEPHONE: (206) 682 8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 16-MAR-1995
APPLICATION NUMBER: US 01
FILING DATE: 16-MAR-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 16-MAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.Ā.
ZIP: WA 98101-2333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/224,831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Renzoni, George E
VATION NUMBER: 37,919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; silarity 100.0%; silarity 100.0%; sometime of the conservative of the conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (206) 224 0779
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Wilbur, D. Scott
Prathare, Pradip M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ss: single
linear
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16-MAR-1995
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Modulating Agents and Methods Related Thereto
47
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Pred. No. 2.5e+05;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                     Sequence 16, Application US/08463480
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06735
FILING DATE: 16-JUL-1993
ATTORNEY AGENT INFORMATION:
NAME: RESNICK, DAVID S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 41956-PCT-US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 617-523-6440
TELEX: STRE UR 2002
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatib
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Vers
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                      APPLICANT: Pastan, Ira H.
APPLICANT: FitzGerald, David J.
TITLE OF INVENTION: Recombinant Pseudomonas
TITLE OF INVENTION: Increased Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 130 W
CITY: BOSTON
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity hes 4; Conserv
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FILING DATE: 17-JAN-1995
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ZIP: 02109
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                                                                                                                                                                                                                                                                                                                                                                                                  1 KDEL 4
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                                                                                                                                                     San Francisco
                                                                                                                                      California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: 617-523-3400
617-523-6440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           2.5e+05;
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                                                                                                                                                                                                                                      Exotoxin with
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:

US 07/901,709

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                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,566B
FILING DATE: 06-JUN-1995
CLASSIFFICATION: 530
PRIOR APPLICATION NUMBER: US 08/463,483
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/463,483
FILING DATE: 05-JUN-1995
PRIOR APPLICATION NUMBER: US 08/314,594
APPLICATION NUMBER: US 08/314,594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tent No.
                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5872212artis Corporation
STREET: 3054 Cornwallis Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15280-36-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/405,615
FILING DATE: 15-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPLICANT:
                                                                                                                                                                                                                                                                                                                                                           CITY: Research Triangle Park
STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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FILING DATE: 18-JUN-1992
                                                                                                                                                                                                                                                                                                                                        COUNTRY:
 APPLICATION NUMBER:
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                 APPLICATION DATA:
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5872212
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Koziel, Michael G
Mullins, Martha A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Duck, Nicholas B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carr, Brian
Desai, Nalini M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nye, Gordon J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kostichka, N. Kristy
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100.0%; Pred. No. 2.5e+05;
US 08/218,018
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Best Local Similarity
Watches 4; Conserve
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                                                                                                              US-08-470-566B-51
                                                                                                                                                                                                                           TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                             NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC1695/CIP3/DIV4 - SQLV4
TELECOMMUNICATION INFORMATION:
                                                                                                                          MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 23-MAR-1994 PRIOR APPLICATION DATA:
                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/037,057 FILING DATE: 25-MAR-1993
                                                                                                                                                                   STRANDEDNESS:
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                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                   l: 4 amino acids amino acids
 KOEL.
                                                       Conservative
                                                                                                                                                       linear
                                                                                                                     .. peptide
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                                                                                                                                                                    single
                                                      100.0%; Score 20; DB 2; L
100.0%; Pred. No. 2.5e+05;
tive 0; Mismatches 0;
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                                                                                   DB 2;
                                                                                Length 4;
                                                       Indels
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                                                       Gaps
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Search completed: August 26, 2003, 16:19:16 Job time : 2.41593 secs

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Result
No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OM protein - protein search, using sw model
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Maximum Match 100%
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB BG
                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                   100.0
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           August 26, 2003, 16:02:18 ; Search time 1.41593 Seconds (without alignments) 372.792 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published Applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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  US-08-765-244-16
US-08-873-601-24
US-09-157-748-3
US-09-157-748-3
US-09-854-122-2
US-09-347-664-35
US-09-333-527-2
US-09-785-921A-16
US-09-785-921A-16
US-09-916-940-28
US-09-916-940-28
US-09-916-940-28
US-09-984-0-28
US-09-980-745-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  497079
Sequence 16, Appl
Sequence 24, Appl
Sequence 30, Appl
Sequence 23, Appl
Sequence 25, Appli
Sequence 27, Appli
Sequence 27, Appli
Sequence 27, Appli
Sequence 28, Appli
Sequence 31, Appli
Sequence 32, Appli
Sequence 33, Appli
Sequence 22, Appli
Sequence 22, Appli
Sequence 22, Appli
Sequence 22, Appli
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15	15	15	15	15	14	14	14	14	14	12	12	12	12	12	12	12	11	11	11	11	11	11	11	10	10	10	10	10	10
\sim	US-10-112-788-18	7-427-	US-10-158-238-17	39-2	1-395-	-10-061-3	0-376-	-801-	-10-	-973-	US-10-066-319-1	-10-252-73;	US-10-226-877A-33	US-10-189-360-42	US-10-177-725-157	-165-	-713-1	US-09-913-238-63	US-09-861-257-19	US-09-906-393A-1	989	US-09-991-209-97	-847-	US-09-925-803-3	US-09-807-721-6	US-09-915-789A-10	US-09-792-630-77	-09-178-286-1	US-09-554-000-49
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
-	18,		•	•	•	25,			9	Ψ		8	33,	42,	157,	150	13,	63,	19,	۲,	24,	97,	•	w L	•		77,	19,	49,
Appl	Appl	Appli	Appl	App1	App1	App1	App1	Appli	Appli	App1	Appli	Appli	Appl	Appl	, App	8, Ap	Appl	App1	, Appl	Appli	App1	Appl	Appli	Appli	Appli	Appl	App1	Appl	Appl

ALIGNMENTS

US-08-765-244-16

Sequence 16, Application US/08765244
Publication No. US20010008771A1
GENERAL INFORMATION:

```
APPLICANT: Seibel, Peter
APPLICANT: Seibel, Andrea
APPLICANT: Seibel, Andrea
TITLE OF INVENTION: CHIMERICAL PEPTIDE-NUCLEIC ACID
TITLE OF INVENTION: FRAGMENT, PROCESS FOR PRODUCING THE SAME AND ITS USES FOR
TITLE OF INVENTION: APPROPRIATELY INTRODUCING NUCLEIC ACIDS INTO CELL ORGANELLES
TITLE OF INVENTION: AND CELLS
FILE REFERENCE: 8484-0018-999
CURRENT APPLICATION NUMBER: US/08/765,244
CURRENT FILING DATE: 1997-10-30
PRIOR APPLICATION NUMBER: PCT/DE95/00775
PRIOR APPLICATION NUMBER: PCT/DE95/00775
PRIOR FILING DATE: 1995-06-11
PRIOR APPLICATION NUMBER: DE P 44 21 079.5
PRIOR FILING DATE: 1994-06-16
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
片
                                         S
                                                                                                                                                                                     US-08-765-244-16
                                                                                        Query Match
Best Local S
Matches 4
                                                                                                                                                                                                                                      LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                   FEATURE:
OTHER INFORMATION: Synthetic sequence
                        1 KDEL 4
1 KDEL
                                                                                     Similarity 100 4; Conservative
                                                                                     100.0%; Score 20; DB 8; 1
100.0%; Pred. No. 4.4e+05;
tive 0; Mismatches 0;
                                                                                                                                    Length 4;
                                                                                          0;
                                                                                          Gaps
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100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0

RESULT 2

US-08-873-601-24

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RESULT 4
US-09-759-960-23
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US-09-157-748-30
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US-09-157-748-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 30, Application US/09157748
Patent NO. US2001003042A1
GENERAL INFORMATION:
APPLICANT: Lorens, James
TITLE OF INVENTION: Multiparameter FACS Assays to Detect Alterations in TITLE OF INVENTION: Cell Cycle Regulation
FILE REFERENCE: A66587/DDB/RMS
CURRENT FILING DATE: 1980-09-21
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                        Sequence 23, Application US/09759960 Patent No. US20010006639A1
                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                             Query Match
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SEQ ID NO 24
LENGTH: 4
TYPE: PRT
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Publication No. US20020064798A1
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                                                                                                     GENERAL INFORMATION:
APPLICANT: Urban,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL: Royal Society London Transaction PAGES: 1-1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Unknown Organism: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Unknown FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH:
           APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
APPLICANT: Collins, Edward J.
APPLICANT: Hedley, Mary Lynn
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
TITLE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
nes 4; Conservative
                                                                                                                                                                                                                                                                                     1 KDEL 4
OF SEQUENCES:
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Pred. No. 4.4e+05;
; Mismatches 0;
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Pred. No. 4.4e+05
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                                                                                                                                                                                                                                                                                                                       0; Indels
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                                                                                                                                                                                                                            FILE REFERENCE: PHA-007.01
CURRENT APPLICATION NUMBER: US/09/854,122
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/202,529
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 51
SOPTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: ALBERTE, RANDALL S.
APPLICANT: SMITH, ROBERT
TITLE OF INVENTION: TRANSGENIC PLANTS INCORPORATING TRAIT OF ZOSTERA MARINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
                                                Query Match
Best Local Similarity
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Patent No. US20020016980A1
                                     Matches
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Best Local Similarity
                                                                                                                  FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/759,960
                                                                                                                                                                                                                   ENGTH:
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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225 Franklin Street
                                   Conservative
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                                                   100.0%; Score 20; DB 9; 100.0%; Pred. No. 4.4e+05;
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100.0%; Pred. No. 4.4e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Paul C
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APPLICANT: Zinke, Holger
TITLE OF INVENTION: Recombinant Fusion Proteins Based on
TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe Viscum
TITLE OF INVENTION: album
FILE REFERENCE: 09283-5
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                                                                                                                                                                                                                             COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DC
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/01
FILING DATE: June 15, 19:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: PAUl CHRISTOU; EVA STROGER; RAINET FISCHER; Carmen MARTIN-VAQUERO; STITLE OF INVENTION: METHODS AND MEANS FOR EXPRESSION OF MAMMALIAN POLYPEPTIDES NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
REGISTRATION NUMBER: 36,669
REFERENCE/DOCKET NUMBER: KL,
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                             NAME: Mary Anne Schofield
                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                               APPLICATION NUMBER: US/09/333,527
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1: 666 Fifth Avenue
New York City
. New York
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100.0%; Pred. No.
/ative 0; Mismatch
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                   KL/JIC 202.1 -
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                                                                             ; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-997-956-2
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                                                                                                                                                 SOFTWARE:
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Patent No. US20020106714A1
GENERAL INFORMATION:
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Matches 4; Conserv
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                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/997,956
CURRENT FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/250,679
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/256,559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Keener, William K.
APPLICANT: Ward, Thomas E.
TITLE OF INVENTION: SELECTIVE DESTRUCTION OF CELLS INFECTED WITH HUMAN
TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS
FILE REFERENCE: LIT-PI-529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/785,921A
CURRENT FILING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                  NUMBER OF
                                                                                                                                                                                                    PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Membrane Molecule Indicator Compositions TITLE OF INVENTION: and Methods FILE REFERENCE: P-NS 5045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (212) 752-5958 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Jalink, Kees
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 4
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                 ING DATE: 2000-12-18
SEQ ID NOS: 8
FastSEQ for Windows Version 4.0
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                               100.0%; Score 20; 100.0%; Pred. No.
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100.0%; Pred. No. 4.4e+05;
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                 Mismatches
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                               4.4e+05;
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; OTHER INFORMATION: Description of Artificial Sequence: endoplasmic; OTHER INFORMATION: reticulum sequence.
US-09-916-940-28
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CURRENT FILING DATE: US/09/727,715
PRIOR APPLICATION NUMBER: US 09/727,715
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 08/963,368
PRIOR APPLICATION NUMBER: US 08/589,109
PRIOR FILING DATE: 1997-01-23
PRIOR APPLICATION NUMBER: US 08/589,911
PRIOR FILING DATE: 1996-01-23
PRIOR APPLICATION NUMBER: US 08/789,333
PRIOR APPLICATION NUMBER: US 08/789,333
PRIOR APPLICATION NUMBER: US 08/787,738
PRIOR FILING DATE: 1997-01-23
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin Ver. 2.0
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Patent No. US20020127564A1

GENERAL INFORMATION:

APPLICANT: No. US20020127564A1an, Garry P

APPLICANT: No. US20020127564A1an, Garry P

TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR

TITLE OF INVENTION: METHODS FOR PEPTIDES AND RNA MOLECULES

FILE REFERENCE: A-64260-6/RMS/AMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ARIAD Gene Therapeutics, Inc.
TITLE OF INVENTION: Regulation of Biological Events Using No. US20020107189A1el Compc
FILE REFERENCE: 374 USD1
CURRENT APPLICATION NUMBER: US/09/781,804
CURRENT FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 64
SOFTMARE: Patentin version 3.0
SEQ ID NO 2
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Patent No. US20020107189A1
GENERAL INFORMATION:
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LENGTH: 4
Query Match
Best Local Similarity
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                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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TYPE: PRT
ORGANIEM: Artificial Sequence
FEATURE:
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  Score 20;
Pred. No.
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  DB 10;
4.4e+05;
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hes 0;
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                     Length 4;
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FILE REFERENCE: 042881/0130
CURRENT APPLICATION NUMBER: US/09/984,183
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 09/457,354
PRIOR APPLICATION NUMBER: 09/457,354
PRIOR FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 60/111,973
PRIOR FILING DATE: 1998-12-11
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 3
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APPLICANT: Lake, Philip
APPLICANT: Wright, Richard M.
APPLICANT: Wright, Richard M.
TITLE OF INVENTION: Anti-CD3 Immunotoxins and Therapeutic Uses Therefor
FILE REFERENCE: CGC 4-31157A/USN
CURRENT APPLICATION NUMBER: US/09/480,236
CURRENT FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
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Best Local Similarity
Matches 4; Conserv
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Patent No. US20020142000A1
GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: LONGENBEKER, MICHAEL B.
TITLE OF INVENTION: MUC-1 ANTAGONIS
TITLE OF INVENTION: DISORDERS
                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: Retrograde OTHER INFORMATION: transport peptide
                                                                                                                                                                                                       FEATURE:
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                                                                        Conservative
                                                                                       100.0%; Score 20; 100.0%; Pred. No.
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APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: TSIEN, ROGER
APPLICANT: TSIEN, ROGER
APPLICANT: TSIEN, ROGER
APPLICANT: GONZALEZ, JESUS
TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY OPTICAL METHODS
FILE REFERENCE: REGEN1290-5
CURRENT APPLICATION NUMBER: US/09/967,772
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US 09/459,956
PRIOR FILING DATE: 1999-12-13
PRIOR APPLICATION NUMBER: US 08/765,860
PRIOR FILING DATE: 1996-12-19
PRIOR APPLICATION NUMBER: PCT/ US96/09652
PRIOR TILING DATE: 1996-06-06
PRIOR APPLICATION NUMBER: US 08/481,977
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US-09-967-772-10
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US-09-999-745-22
Search completed: August 26, 2003, 16:07:07 
Job time : 2.41593 secs
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                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Protein localization sequence US-09-967-772-10
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-999-745-22
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APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA

APPLICANT: Taien, Roger Y.

APPLICANT: Baird, Geoffrey

TITLE OF INVENTION: CIRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS

FILE REFERENCE: REGEN1470-1

CURRENT APPLICATION NUMBER: US/09/999,745

CURRENT FILING DATE: 2001-10-23

PRIOR APPLICATION NUMBER: 09/316,920

PRIOR APPLICATION NUMBER: 09/316,920

PRIOR FILING DATE: 1999-05-21
                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/09967772
Patent No. US20020164577A1
GENERAL INFORMATION:
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Best Local S
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                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH:
                                                                                                                                                                                           y Match 100.0%; Score 20; DB 10; Length 4; Local Similarity 100.0%; Pred. No. 4.4e+05; hes 4; Conservative 0; Mismatches 0; Indels
                                                                                            1 KDEL 4
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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               Pred. No.
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ore greater than or equal to the score of the result being printed,
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1 KDEL 4
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               GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd
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KDEL 31

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	ngth 38; Indels 0; Gaps 0;	iparum) (isolate 427-5) nge 09-Jun-2000 ve polymorphism in T cel ion 1 repeat homology		ngth 35; Indels 0; Gaps 0;	change 25-Oct-1996 eptide (gurmarin) from the		secretory protein rapid lysis III pr hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote probable involveme replication contro hypothetical prote probable ribosomal hypothetical prote
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R.Christie, J.F.; Dunbar, B.; Davidson, I.; Kennedy, M.W. Immunology 69, 596-602, 1990
A;Title: N.terminal amino acid sequence identity between a A;Reference number: A37188; MUID:90243308; PMID:2335378
A;Accession: B37188
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                                                                                                                                                                                                                                                       major body fluid allergen ABA-1 - common roundworm (fragment)
C;Species: Ascaris lumbricoides (common roundworm)
C;Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_chan
C;Accession: B37188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate C;Species: Plasmodium falciparum
C;Date: 03.Jun-1993 #sequence_revision 03.Jun-1993 #text_change 09.Jun-2000
C;Accession: B60657
R;Lockyer, M.J.; Marsh, K.; Newbold, C.I.
Mol. Blochem. Parasitol. 37, 275-280, 1989
A;Title: Wild isolates of Plasmodium falciparum show extensive polymorphism i A;Reference number: A60657; MUID:90114334; PMID:2481827
A;Accession: B60657
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Mol. Biochem. Parasitol. 37, 275-280, 1989
A;Title: Wild isolates of Plasmodium falciparum show extensive
A;Reference number: A60657; MUID:90114334; PMID:2481827
A;Accession: C60657
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C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat
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A; Residues: 1-46 < LEB >
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A; Accession: S39239
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transposase asr7152 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC C.Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC C.Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-200
C.Accession: AH2496
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanaba Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda A,*fitle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyan A; Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AH2496
A;Status: preliminary A;Molecule type: DNA A;Residues: 1-50 KURB
A;Cross-references: GB:BA000020; PIDN:BAB78236.1; PID:g17135690; GSPDB:GNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ornatin E - leech (Placobdella ornata)
(;Species: Placobdella ornata
C;Species: Placobdella ornata
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_cha
C;Accession: S19624
R;Mazur, P.; Henzel, W.J.; Seymour, J.L.; Lazarus, R.A.
Eur. J. Biochem. 202, 1073-1082, 1991
A;Title: Ornatins: potent glycoprotein IIb-IIIa antagonists
A;Reference number: S19566; MUID:92111479; PMID:1765068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cholera enterotoxin chain A2 - Vibrio cholerae (serotype N;Alternate names: CTA2 cholera toxin chain A2 C;Species: Vibrio cholerae
A;Variety: serotype 0139
C;Date: 08-May-1995 #sequence_revision 26-Jul-1996 #text C;Accession: S39239; S39240
R;Lebens, M.; Holmgren, J.
submitted to the EMBL Data Library, November 1993
A;Description: Structure and arrangement of the Cholera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X76390; NID:g433856; A;Experimental source: strain 4260B; serotype C;Superfamily: heat-labile enterotoxin chain P
GB:BA000020; PIDN:BAB78236.1; se: strain PCC 7120
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09-Dec-2002
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Tabata, S.
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R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Accession: E96530
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C;Species: Placobdella ornata
C;Date: 19-Mar-1997 #text_change
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change
C;Accession: S19623
R;Mazur, P.; Henzel, W.J.; Seymour, J.L.; Lazarus, R.A.
Eur. J. Biochem. 202, 1073-1082, 1991
  RESULT
A35416
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A;Genome: plasmid
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                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-54 <ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F13F21.16 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
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Best Local
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;Residues: 1-52
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100.0%; Pred. No. 2.6e+02;
Mismatches 0;
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Pred. No. 2.5e+02;
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Cross-references: GB:BA000019; PIDN:BAB76352.1; PID:g17133790; GSPDB:GN00179
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R;Austin, C.A.; Barot, H.A.; Margerrison, B.E.C.; Turcatti, G.; Wingfield, P.; Hayes, M.N. Blochem. Blophys. Res. Commun. 170, 763-768, 1990
A;Title: Structure and partial amino acid sequence of calf thymus DNA topoisomerase II: <a href="https://doi.org/10.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc.1001/j.nc
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; erage, G.; Gillet, W.; Grant, C.; Guenthmer, D.; Kutyavin, T.; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan,
                                                                                                                Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yas
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE2387
                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein asr4653 [imported] - Nostoc sp. (strain PCC 7120) (;Species: Nostoc sp. PCC 7120 c;Species: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec C;Accession: AE2387
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A;Residues: 1-58 <AUS>
C;Keywords: isomerase
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                                                                                                                                                                                                                                                                                            R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada
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A;Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) II - bovine (fragments)
A;Molecule type: DNA
A;Residues: 1-60 <KU
                                                                                 A;Status: preliminary
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;Experimental source: strain C58 (Dupont)
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, M.; Yasuda, I
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09-Dec-2002
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Tabata, S.
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C;Pate: 19-Mar-1yy, "C;C;Pate: 19-Mar-1yy, "C;Accession: S11883; Palchaudhuri, S.
R;Banerjee, A.; Weber, P.C.; Palchaudhuri, S.
Mol. Gen. Genet. 220, 320-324, 1990
Mol. Gen. Genet. 220, 320-324, 1990
A;Title: Comparison of the CopB systems of plasmids R1 and Colv2-K94: a single base alteral particular and the CopB systems of plasmids R1 and Colv2-K94: a single base alteral particular and particular and colv2-K94: a single base alteral particular and colv2-K9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
$11883

copB protein - Escherichia coli plasmid ColV2-K94

C;Species: Escherichia coli
C;Sate: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 30-May-1997
                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: copB
A;Genome: plasmid ColV2-K94
C;Superfamily: repA2 protein
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A;Residues: 1-62 <KLE>
A;Cross-references: GB:AE001028; GB:AE000782; NID:g2689351; PIDN:AAB90163.1; PID:g264951
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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        GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
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S10D HUMAN
SECE SYNY3
VR3 BPT4
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CPB3 ECOLI
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Q57687 methanococc
P03855 escherichia
P13320 bacteriopha
P07079 bacteriopha
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P02402 artemia sgrachocyst
Q58474 mycobacteri
Q58474 methanococc
Q2948 arabidopsis
Q46244 clostridium
P44589 haemophilus
Q46419 fagopyrum e
Q58419 fagopyrum e
Q58419 methanococc
Q07090 nicotiana t
Q43636 ricinus com
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P25512 placobdella
O29187 archaeoglob
P25186 bacteriopha
Q9hsu8 halobacteri
P51727 bacteriopha
P29377 homo sapien
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P08807 human immun
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GUR GYMSY ID GUR_GYMSY STANDARD; PRT; 35 AA. AC P25810; DT 01-PEB-1994 (Rel. 22, Created) DT 01-FEB-1994 (Rel. 28, Last sequence update) DT 15-SEP-2003 (Rel. 42, Last annotation update) DE Gurmarin (Sweet-taste-suppressing peptide). OS Gymnema sylvestre (Gurmar). OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; OC Asteridae; lamiids; Gentianales; Apocynaceae; Periplocoideae; OC Gymnema. OX NCBI_TaxID-4068; RP SEQUENCE. RC TISSUE=Leaf;	1 Similarity 100.0%; Pred. No. 65; 4; Conservative 0; Mismatches 0; Indels 1 KDEL 4	NCE: INE=92111479; PubMed=1765068; (P., Henzel W.J., Seymour J.L., Lazarus R.A.; atins: potent glycoprotein IIb-IIIa antagonists and p gation inhibitors from the leech placobdella ornata. J. Biochem. 202:1073-1082(1991). PUNCTION: POTENT INHIBITOR OF FIBRINOGEN INTERACTION RECEPTORS EXPRESSED ON GLYCOPROTEIN IIB-IIIA COMPLEX. BLOOD FROM CLOTTING DURING EITHER FEEDING AND/OR STOR RIGESTED BLOOD. SIMILARITY: BELONGS TO THE ORNATIN FAMILY. PFO2088; Ornatin; 1. PF02088; Ornatin; 1. PF02088; Ornatin; 1. Coapilation; Platelet; Cell adhesion. EER 28 28 28 28 28 28 28 28 28 28 28 28 28 2	ND SUI	34 20 100.0 118 1 V118 ASFB7 25 100.0 120 1 RL31_PICMA 26 20 100.0 121 1 PFDB METTH 27 100.0 121 1 PFDB METTH 28 20 100.0 123 1 RL7A_METKA 29 100.0 123 1 RL7A_METKA 20 100.0 123 1 RL7A_METTH 39 20 100.0 123 1 RT31_YEAST 40 20 100.0 123 1 RT31_YEAST 41 20 100.0 126 1 RX12_CYAPA 42 20 100.0 127 1 UCR7_YEAST 43 20 100.0 128 1 RL7_COXAPA 44 20 100.0 129 1 RSB_ECOLI 45 20 100.0 129 1 RSB_HAEIN 46 20 100.0 130 1 RSB_BUCAK 47 20 100.0 129 1 RSB_BUCAK 48 20 100.0 130 1 RSB_BUCAK 49 20 100.0 130 1 RSB_BUCAK 40 20 100.0 130 1 RSB_BUCAK 41 20 100.0 130 1 RSB_BUCAK 42 20 100.0 130 1 RSB_BUCAK 43 20 100.0 130 1 RSB_BUCAK 44 20 100.0 130 1 RSB_BUCAK 45 20 100.0 130 1 RSB_BUCAK
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01-NOV-1997
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SEQUENCE
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Eur. J. Biochem. 264:525-533(1999).

FUNCTION: SUPPRESSES STRONGLY THE SWEET TASTE RESPONSES IN THE RAT WITH HIGH SPECIFICITY TO SUCROSE, GLUCOSE, GLYCINE, AND SACCHARIN. WITH HIGH SPECIFICITY TO SUCROSE, GLUCOSE, GLYCINE, AND SACCHARIN. THIS EFFECT IS REVERSIBLE, BUT COMPLETE RECOVERY OF THE SUPPRESSED RESPONSES REQUIRED AT LEAST 3H. GURMARIN SHOWED NO EFFECT OR ONLY A VERY WEAK EFFECT ON THE SWEET TASTE SENSATION IN HUMANS.
                                                                                                SEQUENCE FROM N.A.
MEDLINE=88281278; PubMed=3395517;
                                                                                                                                               Human immunodeficiency virus type 1 (2-6 Viruses; Retroid viruses; Retroviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kamei K., Takano R., Miyasaka A., Imoto T., Hara S.;
"Amino acid sequence of sweet-taste-suppressing peptide (gurmarin)
from the leaves of Gymnema sylvestre.";
                                                                                Gallo R.C
                                                                                                                                    NCBI_TaxID=11681;
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J. Biomol. N
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Aimoto S., Akasaka K.;
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                                                                   "Nucleotide sequence analysis of the
                                                                                        Yourno J., Josephs S.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Taste-modifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "High-resolution solution structure of gurmarin,
                                                        solate of HIV-1.";
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                                                                                                                                                                                 protein
S Res. Hum. Retroviruses 4:165-173 (1988). FUNCTION: ACTS IN THE DEGRADATION OF CD4 IN RETICULUM AND IN THE ENHANCEMENT OF VIRION R MEMBRANE OF INFECTED CELLS.
SUBCELLULAR LOCATION: Membrane-bound.
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1C4E; 27-AUG-99.
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ngley A.J., Smith
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otein) (Fragment).
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Pred. No.
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lae; Lentivirus.
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01-MAY-1992
28-FEB-2003
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Mazur P., Henzel W.J., Seymour J.L., Lazarus R.A.;
"Ornatins: potent glycoprotein III-IIIa antagonists and platelet aggregation inhibitors from the leech placobdella ornata.";
Eur. J. Blochem. 202:1073-1082(1991).
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                                                                                                    SEQUENCE
                                                                                                                                     InterPro; IPR002463; Ornatin. Pfam; PF02088; Ornatin; 1. ProDom; PD012062; Ornatin; 1.
                                                                                                                                                                          PIR; S19624; S19624.
                                                                                                                                                                                                                                                                                                                                        Placobdella ornata (Turtle leech).
Bukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Rhynchobdellida; Glossiphoniidae; Placobdella.
NCBI_TaxID=6415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIV; J03653; VPU$JY1.
InterPro; IPR002094; Vpu.
Pfam; PF00558; Vpu; 1.
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P25514;
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                                                                                                                                                                                                                FUNCTION: POTENT INHIBITOR OF FIBRINOGEN INTERACTION WITH PLATELET RECEPTORS EXPRESSED ON GLYCOPROTEIN IIB-IIIA COMPLEX. MAY PREVENT BLOOD FROM CLOTTING DURING EITHER FEEDING AND/OR STORAGE OF
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22, Last sequence 41, Last ann
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44 CELL ATTACHMENT SITE
5727 MW; 688408EB1E001B92 CRC
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01-MAY-1992
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28-FEB-2003
                                                                                                                                                                           Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Ketchum K.A., Dodson R.J., Gainn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kikkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B. Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhd Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T. Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
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Placobdella ornata (Turtle leech).
Placobdella ornata (Turtle leech).
Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Rhynchobdellida; Glossiphoniidae; Placobdella.
NCBI_TaxID=6415;
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Mazur P., Henzel W.J., Seymour J.L., Lazarus R.A.;
"Ornatins: potent glycoprotein IIb-IIIa antagonists and platel.
aggregation inhibitors from the leech Placobdella ornata.";
Bur. J. Biochem. 202:1073-1082(1991)
-i- FUNCTION: POTENT INHIBITOR OF FIBRINOGEN INTERACTION WITH:
RECEPTORS EXPRESSED ON GLYCOPROTEIN IIB-IIIA COMPLEX. MAY
BLOOD FROM CLOTTING DURING EITHER FEEDING AND/OR STORAGE O
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SITE 42 44 CELL ATTACHMENT SITE.
SEQUENCE 52 AA; 5845 MW; BA55CA7408EF4F09 CRC64;
  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=VC-16 / DSM 4304 / ATCC 49:
MEDLINE=98049343; PubMed=9389475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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NCBI_TaxID=2234;
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Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
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390:364-370(1997).
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fulgidus.";
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Hypothetical protein; Cor
                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                Kutter E., Arisaka F., Kunisawa T., Tsugita A., Mosig G., Mesyanzhinov V., Ruger W., Stidham T., Thomas E.; "Batteriophage T4 genome analysis.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                 Daegelen P., Brody E.;
"The rIIA gene of bacteriophage T4. I. Its DNA sequence and discovery of a new open reading frame between genes 60 and rIIA.";
Genetics 125:237-248(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteriophage T4.
Viruses; dsDNA viruses,
T4-like viruses.
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01-MAY-1992 (Rel. 22, Last sequence update)
01-MAY-1992 (Rel. 22, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical 8.1 kDa protein in rIIA-Gp60 intergenic region.
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                                                                                                                    PIR; JU0399; JU0399.
Hypothetical protein.
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MEDLINE=90337270; PubMed=2379817;
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AF158101; AAD42648.1; -.
52
                         1 KDEL 4
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                                                   Similarity 4; Conserv
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85 MW; E2F541BA57A10477 CRC64;
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                                                               Score 20; DB 1;
Pred. No. 1.6e+02;
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RESULT 8 Y066_HALN1 ID Y066_HALN1

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P51727;
01-OCT-1996
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Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L.,
Benome sequence of Halbacterium species NRC-1.",
"Genome sequence of Halbacterium species NRC-1.",
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
-i- SIMILARITY: BELONGS, TO THE UPF0175 FAMILY.
                                                   MEDLINE=85128433; PubMed=6098523; Benjamin R.C., Fitzmaurice W.P., Huwarice W.P., Huwarice of cloned DNA influenzae bacteriophage HPIcl."; Gene 31:173-185(1984).
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16-OCT-2001
16-OCT-2001
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Viruses; dsDNA vir
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Hypothetical protein; Complete
SEQUENCE 76 AA; 8577 MW; 40
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  MEDLINE=96279738;
                                                                                                                            STRAIN=HP1C1;
                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                    NCBI_TaxID=10690;
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Archaea; Euryarchaeota; Halobacteria;
Halobacteriaceae; Halobacterium.
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             STRAIN=HP1C1
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InterPro; IPR005368; UPF0175.
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4083E6DCFA66C87B CRC64;
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Pred. No. 1.8e+02;
; Mismatches 0;
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                                                                                Huang P.C.,
NA segments
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                                                                                , Scocca J.J.;
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MEDLINE=92304291; Publ
Howard A., Legon S.,
"Molecular cloning an
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P29377;
01-DEC-1992
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                                      Waldman A.S., Scocca J.J.;
"The complete nucleotide sequence of bacteriophage HP1
Nucleic Acids Res. 24:2360-2368(1996).
-!- FUNCTION: INDUCES HOST CELL LYSIS BY CAUSING FORMAY
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the MWBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                Jeung E.B., Krising
                                                                                                                                                        calbindin-D9k."
                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=92354716; PubMed=1379540;
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TRANSMEM 8 ;
SEQUENCE 78 AA; 80
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Mammalia; Eutheria;
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28-FEB-2003
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Waldman A.S.,
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                                                                                                                                             307:224-228(1992).
                                                                                                                                                                                                                                                                                                                                                          Krisinger J., Dann J.L., I cloning of the full-length
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S., Spurr N.K., Walters J.R.I
g and chromosomal assignment
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; Primates;
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0; Mismatches
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3FC0596BE0AE4FED
                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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h cDNA
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RESULT 11
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InterPro; IPR002048; EF-hand.
Pfam; PF00036; efhand; 1.
Pfam; PF01023; S_100; 1.
ProDom; PD0003407; CaBP S100; 1.
ProDom; PD000012; EF-hand; 1.
PROSITE; PS00018; EF HAND; 1.
PROSITE; PS00018; ST0_CABP; 1.
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EMBL; L13220; AAA35638.1;
EMBL; L13042; AAA35637.1;
PIR; JN0246; JN0246
HSSP; P02632; 1CB1
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yanada M., Yasuda M., Tabata S.; "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).

-I- SUBCZILUILAR LOCATION: Tail-anchored membrane protein (Potential) -i- SUBCZILUILAR LOCATION: Tail-anchored membrane protein (Potential) -i- SIMILARITY: Belongs to the secS/SEC61-gamma family.
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                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93281410; PubMed=7685084;
Schmidt J., Subramanian A.R.;
"Sequence of the cyanobacterial tRNA(w)
6803: requirement of enzymatic 3' CCA au
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16-OCT-2001
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01-OCT-1994
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ACETYLATION (BY SIMILARITY).

EF-HAND 1 (LOW AFFINITY).

EF-HAND 2 (HIGH AFFINITY).

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P17309;
01-AUG-1990
01-OCT-1993
28-FEB-2003
                                                                                                                                                                        Nucleic Acids |
[3]
                                     MEDLINE=94063508; PubMed=8244025; Raudonikiene A., Nivinskas R.; "The sequences of gene rIII of Gene 134-135"
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                                                                                                                          SEQUENCE FROM N.A., AND CHARACTER MEDLINE=92207389; PubMed=1587487; Raudonikiene A., Nivinskas R.; "Gene_rIII is the nearest downstr
                                                                                                                                                                                 MEDLINE=90332452; PubMed=2377483;
Raudonikiene A., Nivinskas R.;
"Nucleotide sequence of bacteriophage
Nucleic Acids Res. 18:4280-4280(1990).
                                                                                                                                                                                                                                                              Prilipov A.G., Mesyanzhinov V.V., Aebi U. "Cloning and sequencing of bacteriophage positions 128.3-130.3.";
                                                                                                                                                                                                                                                                                    STRAIN=D;
MEDLINE=90301484; PubMed=2362813;
Meavanzhinov V.V.,
                                                                                                                                                                                                                                                                                                                                                                                        Protein rIII.
RIII OR 31.-1.
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EMBL; D90906; BAA17421.1; -.
PIR; S77318; S77318.
  SEQUENCE FROM N.A.
Kutter E., Arisaka
                                    "The sequences of gene
Gene 134:135-136(1993).
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=D;
                                                                                                                                                                                                                                                                                                                                                       T4-like viruses
                                                                                                      Gene 114:85-90(1992).
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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InterPro; IPR005807;
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                                                of bacteriophage
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   Tsugita A.,
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MEDLINE=96337999; pubMed=8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Coverbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus

jannaschii.";
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EMBL; U67479; AAB98227.1; PIR; D64329; D64329.
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EMBL; M37882; AAA32507.1; -.
EMBL; X54536; CAA38406.1; -.
EMBL; AF158101; AAD42650.1; -.
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Methanocaldococcaceae; Methanocaldococcus.
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Nucleic
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SEQUENCE FROM N.A.
SPECIES=E.coli; PLASMID=IncFII R1-19 (R1 drd-19);
MEDLINE=81172236; PubMed=6261081;
Medline=81172236; PubMed=81172236; PubMed=81172236; PubMed=81172236; PubMed=81172236; PubMed=81172236; PubMed=81172236; PubMed=81172236; PubMed=81172236; Pu
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                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang Y.
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., C
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding H
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
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SEQUENCE 82 AP
                                                                                                                                                       EMBL; AF386526; AAL72557.1; -. PIR; A04484; WMEC5R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The nucleotide sequence of the replication control region of the resistance plasmid R1drd-19."; Mol. Gen. Genet. 181:116-122(1981).
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Plasmid IncFII R1-19 (R1 drd-19),
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REPA2 OR COPB OR REPB OR CP0258.
                                                                                                                                                                                                                                                                                                                                                                                                                             ough comparison with genomes of Escherichia coli K12 and O157." leic Acids Res. 30:4432-4441 (2002).
FUNCTION: THIS PROTEIN IS INVOLVED IN THE DETERMINATION OF COPNUMBER IN GENE REPLICATION. IT BINDS TO THE REPA PROMOTER THUS INHIBITING THE SYNTHESIS OF THE MRNA FOR THE INITIATOR PROTEIN
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                     Similarity
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2272406; PubMed=12384590;
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Wu H., Qu [
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=91203817; PubMed=2017138;

Gansz A., Kruse U., Rueger W.;

Gansz A., Kruse U., Rueger W.;

"Gene product dsbA of bacteriophage T4 binds to late promoters and enhances late transcription.";

Mol. Gen. Genet. 225:427-433(1991).

-i- FUNCTION: TOTAL TO
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P13320;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Doubles tranded binding protein (DsDNA binding protein A).
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Kutter E., Arisaka F., Kunisawa T., Tsugita A., Mosig G.,

Mesyanzhinov V., Ruger W., Stidham T., Thomas E.;

"Bacteriophage T4 genome analysis.";

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
T4-like viruses.
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Local Similarity 100.0%; Pred. No. 2.1e+02;
hes 4; Conservative 0; Mismatches 0; Indels
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Q9eqe6 mus musculu
Q8drv6 streptococc
Q9ng47 aedes albop
Q57372 vibrio chol
Q9dd7 homo sapien
Q8eb07 shewanella
Q50051 mycobacteri
Q8st38 anartia fat
Q9svf9 dryas iulia
Q8yky6 anabaena sp
Q8t5e2 anartia lyt
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Q9e8d1 gymnema syl
Q13833 homo sapien
Q13832 homo sapien
Q06527 lactobacill
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RESULT 2 Q9S8D1 ID Q9S8D1 PRELIMINARY; PRT; 35 AA.	Qy 1 KDEL 4 Db 9 KDEL 12	Query Match 100.0%; Score 20; DB 11; Length 21; Best Local Similarity 100.0%; Pred. No. 3.8e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0	FI NOW TEK 21 21 SQ SEQÜENCE 21 AA; 2627 MW; 0820P760BC776F9A CRC64;	NON TER 1	EMBL; AJ278768;	gene structure, and sequence similarities to molybden	Ramming M. Kins S. Werner N. Hermann A. Betz H.	RY MEDITUE=20420367: PubMed=10963686:	NCBI TaxID=10090:	OC Euxaryota; Metazoa; Chordata; Cfanrata; Vertebrata; Eutereoscomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	Mus musculus (Mouse).	Gephyrin (Fragment).	DT 01-OCT-2002 (TEMBIFE). 22, Last annotation update)	01-MAR-2001 (TrEMBLrel. 16, Creat	Q9ESX0;	ID Q9ESX0 PRELIMINARY; PRT; 21 AA.	ODDICKO	ALIGNMENTS	
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EMBL; X91664; CAA62852.1; -.
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Q13833; PRELIMINARY; PRT; 40 AA.
Q13833; Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-DCC-2001 (TrEMBLrel. 19, Last annotation update)
B2 bradykinin receptor basal promoter, allele BP-58-T (Fragment).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Biosci. Biotechnol. Biochem. 59:1956-1957(1995)
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Ota M., Ariyoshi Y.;
"Location of the disulfide bonds of the sweetness-suppressing
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Gymnema sylvestre,

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; lamiids; Gentianales; Apocynaceae; Periplocoideae; Gymnema.
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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01-MAY-2000
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Pred. No. 6.2
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n the promoter region of the human
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SEQUENCE
                                                                                                                                                                                                     "The bspA locus of Lactobacillus fermentum uptake system.";
                                                                                                                                                                                                                                                                                                           MEDLINE=97294473; PubMed=9150229;
Turner M.S., Timms P., Hafner L.M., G
"Identification and characterization
protein from Lactobacillus fermentum
J. Bacteriol. 179:3310-3316(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-UUL-1997 (TrEMBLrel. 04, Created)
01-UUL-1997 (TrEMBLrel. 04, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last sequence update)
Cystathionine gamma-lyase homolog (Fragment).
Lactobacillus fermentum.
Bacteria, Firmicutes; Lactobacillales; Lactobacil
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NON_TER
VARIANT
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MEDLINE=96209920; PubMed=8655154;
Braun A., Maier E., Kammerer S., Mueller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A novel sequence polymorphism bradykinin B2-receptor gene."; Hum. Genet. 97:688-689(1996).
                                                                                                                                                 InterPro; IPR000277; Cys_Met_Meta_PP
pfam; PF01053; Cys_Met_Meta_PP; 1.
                                                                                                                                                                                J. Bacteriol. 181:2192-2198(1999)
EMBL; U97348; AAC45329.1; -.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 7.3
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RESULT 6
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RESULT 8
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01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-UA159 / ATCC 700610 / Serotype C;
MEDLINE=22295063; PubMed=12397186;
Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Ajdic D., McShan W.M., Tian R., Kenton S., Jia H., Lin S.,
Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S.,
Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti
"Genome sequence of Streptococcus mutans UA159, a cariogenic o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Durkin M.E., Keck-Waggoner C.L., Popescu N.C., Thorgeirsson S.S., "Integration of a c-myc Transgene Results in Disruption of the Mouse Gtf2irdl Gene, the Homologue of the Human GTF2IRDl Gene Hemizygously Deleted in Williams-Beuren Syndrome.";
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
General transcription factor II-I repeat domain protein
Q9NG47
                                                                                                                                                                                                                                                                                                               Proc. Natl Acad. Sci. U.S.A. 99:14434-14439(2002).
EMBL; AE015032; AAN59699.1; -
Hypothetical protein; Complete proteome.
SEQUENCE 41 AA; 4849 MW; CD8F7DC062E6D60B CRC64;
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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EMBL; AF257477; AAG44656.1; -.
MGD; MGI:1861942; Gtf21rd1.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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01-MAR-2001
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Pred. No. 7.3e+02;
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Yang F.F., Zhao T.T., Li D.D.;

Yang F.F., Zhao T.T., Li D.D.;

Yang F.F., Zhao T.T., Li D.D.;

Pulfferentialy expressed genes of Ae

"Differentialy expressed genes of Ae

"Ith dengue-2 virus.";

Submitted (MAY-2000) to the EMBL/Gen

EMBL; AF263471; AAF73440.1; -

InterPro, IPR000235; Ribosomal S7; 1.

ProDom; PD000817; Ribosomal S7; 1.
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01-NOV-1996
01-NOV-1996
01-MAR-2003
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O1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-OCT-2000 (TrEMBLrel. 21, Last annotation update)
fil-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Ribosomal S5 protein (Fragment).
Aedes albopictus (Forest day mosquito).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cholerae 0139.";
FEMS Microbiol. Lett. 117:197-202(1994).
EMBL; X76391; CAA53975.1; -.
EMBL; X76390; CAA53974.1; -.
HSSP; P01555; 1XTC.
   Q9UDJ7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94237453; PubMed=8181723;
Lebens M., Holmgren J.;
"Structure and arrangement of the cholera toxin genes in Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria;
Vibrionaceae; Vibrio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001144; Enterotoxin_A.
InterPro; IPR000886; ER target.
Pfam; PP01375; Enterotoxin_A; 1.
PROSITE; PS00014; ER TARGET; 1.
SEQUENCE 46 AA; 5447 MW; 1B6085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                     Local Similarity nes 4; Conserv
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
Nucleolar shuttle protein B-23=38 kDa major NOS-binding
                                                                                                                                                                         TIGR; SO3729; -...
Hypothetical protein; Complete proteome.
SEQUENCE 49 AA; 5340 MW; 7ABE848EADOFFAB0 CRC64;
                                                                                                                                                                                                                                                  Shewanella oneidensis.";
Nat. Biotechnol. 20:1118-1123(2002).
EMBL; AE015806; AAN56713.1; -.
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SEQUENCE
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Adachi Y., Copeland T.D., Hatanaka M., Oroszlan S.;
"Nucleolar targeting signal of Rex protein of human T-cell leukemia
virus type I specifically binds to nucleolar shuttle protein B-23.";
J. Biol. Chem. 268:13930-13934(1993).
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8.5e+02;
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Best Local S
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01-JUN-2002
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01-NOV-1996
01-NOV-1996
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                                                                                                                                                                                                                                            NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Blum M.J., Bermingham E., Dasmahapatra K.;

"A Molecular Phylogeny of the Neotropical Butterfly Genu
"A Molecular Phylogeny of the Neotropical Butterfly Genu
(Lepidoptera: Nymphalidae).";

Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AY038684; AAM03332.1; -.

EMBL; AY038685; AAM03333.1; -.

InterPro, IPR000652; Triophos_ismrse.

Pfonlon; PF00121; TIM; 1.

ProDom; PD001005; Triophos_ismrse; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Papilionoidea; Nymphalidae; Nymphalinae; Anartia.
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Corynebacterineae; Mycoba
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                                                                                                                                                   Score 20;
Pred. No.
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RESULT Q95VF9

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RESULT 15
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QBYKY
AC QBYKY
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Best Local Similarity
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SEQUENCE FROM N.A.

MEDLINE-21595285; PubMed=11759840;

Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,

Wateanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,

Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,

Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,

Yasuda M., Tabata S.,

"Complete genomic sequence of the filamentous nitrogen-fixing

Cyanobacterium Anabaena sp. strain PCC 7120.";

DNA Res. 8:205-213(2001).

EMBL; AP003600; BAB78236.1; -.

EMBL; AP003600; BAB78236.1; -.
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01-MAR-2002
01-MAR-2002
01-MAR-2002
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STRAIN-STRI-B-293-Tpi-1;
Beltran M.S. Jiggins C.D., Bull V., McMillan O., Bermingham E.,
Beltran M.S. Jiggins C.D., Bull V., McMillan O., Bermingham E.,
Beltran M.S. Jinares M.;
"Phylogenetic discordance at the species boundary: comparative gene
genealogies between Heliconius butterflies.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
BMBL; AF413797; AAL08558.1;
InterPro; IPR000622; Triophos_ismrse.

Pfam; PF00121; TIM; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anabaena sp. (strain PCC 7120).
Plasmid pCC7120alpha.
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
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Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Papillonoidea; Nymphalidae; Heliconiinae; Dryas.
                                                                                                                                                                                                                                                               Plasmid; Complete proteome. SEQUENCE 50 AA; 5760 MW;
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KDEL 11
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(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
                                                                                                                              Conservative
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5394 MW;
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Pred. No. 8.9e+02;
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Search completed: August 26, 2003, 16:09:20 Job time <7.31858 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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1: gb ba:*
2: gb htg:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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em htgo_nus:*
em htgo_nus:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

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PN JP 2002
PD 10-SEP-
PF 05-MAR-
PI TAKESHI
PI SUGIMOT
PI ICHIRO
PC C12N15/
G001033/577/
PC C12P21/
PC C12P21/
PC C12P21/
PC H Key
FT SOURCE
                                                                                                                                                                                                                                               Human herpesvirus 5
Human herpesvirus 5
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                              Draper,K.G., Mcswiggen,J.A., Holecek,J.J., Dudycz,L.W., Macejak,D.G. and Mamone,J.A. Methojak,D.G. and mone of the control of 
                                                                                                                                                                                                                                                                                                                                                                          Sequence 237 from Patent AX710937
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Matsumura,T., Yohoda,N., Ito,K., Kato,M., Sugimoto,C., Ueda,I.,
Ohashi,K. and Li,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BD174826.1 GI:29120518 JP 2002253262-A/12. unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibody-producing transgenic plant
Patent: JP 2002253262-A 12 10-SEP-2002;
KK SCIENCE TANAKA, HOKKAIDO GREEN BIO INSTITUTE, CHIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unclassified
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C12N15/09, A01H5/00, C07K16/08, C12N5/10, C12Q1/70, G01N33/569,
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TAKESHI MATSUMURA, NORIKO YOHODA, KEIZO ITO, MIHOKO KATO, CHIHIRO
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10-SEP-2002
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/db_xref="taxon:32644"
1 c 3 g
    /organism="Human herpesvirus
/mol_type="genomic RNA"
'mol_type="genomic
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14-MAY-1992 US 07/88283,14-MAY-1992 US 07/8828

14-MAY-1992 US 07/882886,14-MAY-1992 US 07/8828

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14-MAY-1992 US 07/93738,26-AUG-1992 US 07/9881

31-JUL-1992 US 07/93738,26-AUG-1992 US 07/9358

26-AUG-1992 US 07/93738,26-AUG-1992 US 07/9481

15-OCT-1992 US 07/936322,07-DEC-1992 US 07/9481

15-OCT-1992 US 07/937130,07-DEC-1992 US 07/9871

77-DEC-1992 US 07/987130,07-DEC-1992 US 07/9871

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77-DEC-1992 US 07/987130,07-DEC-1992 US 07/9871

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Method and reagent for inhibiting viral replication Patent: JP 200342285-A 238 12-DEC-2000;
RIBOZYME PHARMACEUTICALS INC
OS Artificial Sequence
ON APT 200342285-A/238
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C12N15/09, C12N5/10, C12N7/00, C12N9/22//(C12N5/10, C12R1:91),
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15 - OCT - 1992 US
26 - AUG - 1992 US
27 - DEC - 1992 US
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CC
FH Key
FT source
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PI JAMES J HOLESEK, ANTHONY J MAMONE
PC C12N15/09, C12N5/10, C12N7/00//A61K38/43, A61K39/1:
PC A61K39/135,
PC A61K39/145, A61K39/21, A61K39/23, A61K39/245, A61K39
PC A61F31/16, A61F31/16, A61F31/18, A61F31/22, A61F35/PC
PC A61F31/14, A61F31/16, A61F31/18, 
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JP 2000342286-A/238.
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C12N15/09,C12R1:93),C12N15/00,C12N5/00,A61K37/48,(C12N15/00,)
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A61K39/145,A61K39/21,A61K39/23,A61K39/245,A61K39/29,A61K48/00,
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C12N15/09,C12N5/10,C12N7/00//A61K38/43,A61K39/125,A61K39/13,
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Location/Qualifiers
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07/882886, 14-MAY-1992 US
07/882886, 14-MAY-1992 US
07/882889, 14-MAY-1992 US
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07/88289, 14-MAY-1992 US
07/882849, 14-MAY-1992 US
07/884074, 14-MAY-1992 US
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07/884436, 14-MAY-1992 US
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07/963322,07-DEC-1992
07/987130,07-DEC-1992
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Method and reagent for the modulation and dia
nogo gene expression
Patent: WO 0159103-A 653 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt,
McSwiggen, James (US); Chowrira, Bharat M.
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Method and reagent for the modulation and di
nogo gene expression
Patent: WO 0159103-A 652 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt,
McSwiggen, James (US); Chowrira, Bharat M.
Location/Qualifiers
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Sequence 652 from Patent WO0159103
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           /organism="synthetic construct"
/mol type="mRNA"
/db_xref="taxon:32630"
/noTe="Nucleic Acid"
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AX215212/c
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Patent: WO 0159103-A 654 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
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Sequence 654 from Patent W00159103.
AX215212
AX215212.1 GI:15525255
Blatt,L., Mcswiggen,J. and Chowrira,B.M.
Method and reagent for the modulation and diagnosis of cd20 and gene expression
Patent: WO 0159103-A 1501 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
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/mol_type="mRNA"
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1 (bases 1 to 20)
Marchetti, A., Buttitta, F.,
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ROSCHER ADELBERT (DE)
Other publication DE 19518931 960919
Location/Qualifiers
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                         1 (bases 1 to 20)
Bennett, C.F. and Cowsert, L.M.
Antisense modulation of calreticulin expression
Patent: US 6426220-A 66 30-JUL-2002;
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Marchetti, A. Buttitta, F., Smith, G.H. and Callahan, R. Nuccleotide and deduced amino acid sequences of tumor gene Patent: US 6342392-A 16 29-JAN-2002;

Location/Qualifiers
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Sequence 16 from patent
AR183981
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Bennett, C.F. and Cowsert, L.M.
Antisense modulation of calreticulin expression
Patent: US 6426220-A 68 30-JUL-2002;
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Bennett, C. F. and Cowsert, L.M.
Antisense modulation of calreticulin
Patent: US 6426220-A 67 30-JUL-2002;
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1 (bases 1 to 20)

1 (bases 1 to 20)

Miraglia, L.J., Nero, P., Graham, M.J., Monia, B.P. and Cowsert, L.M.

Miraglia, L.J., Nero, P., Graham, M.J., Monia, B.P. and Cowsert, L.M.

Antisense modulation of human MDM2 expression

Patent: JP 2002508944-A 229 26-MAR-2002;

ISIS PHARMACEUTICALS INC

OS Unidentified

PN JP 2002508944-A/229

PN JP 2002508944-A/229

PD 26-MAR-1999 US 09/048810

PR 26-MAR-1998 US 09/048810

PR 26-MAR-1998 US 09/048810

PR 26-MAR-1998 US 09/048810

PR 26-MAR-1998 US 09/048810
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Antisense modulation of human MDM2 expression FH Location/Qualifiers
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C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04//
C12Q1/68,
C12N15/00
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Location/Qualifiers
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-DB=N Geneseq_19Jun03 -QFMT=fastap -SUFFIX=rng -NINMATCH=0.1 -LOOPCL=0
-DBN Geneseq_19Jun03 -QFMT=fastap -SUFFIX=rng -NINMATCH=0.1 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALICN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HAPRISIZE=500 -MINLEN=0 -MAXIEN=20000000000
-USER=USO9696872_@CGN_1_1_0_@runat_26082003_151137_3213 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGILOG
-DBV TIMEDUT=120 -WARN ITMEOUT=30 -THREADS=1 -XGAPDOP=10 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPDEXT=0.5 -DELOP=6 -DELEXT=7
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Pred. No. is the number of results predicted by chance score greater than or equal to the score of the result to have a being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1		45	4	C 43		41	40	39	38	37		c 35		ယ္	32	31	30	2 6	ى ت	27	26	25		c 23	-		c 20		C 18		7 5		C 13		c 11	10	ი 9		c 7	6	ი თ,	4 (۽ ند	ىر ر		Result No.
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AAZ35104

AAZ35104 standard; DNA; 12 BP.

AAZ35104;

13-MAR-2000 (first entry)

DNA encoding endoplasmic reticulum retention signal.

Endoplasmic reticulum; retention signal; monocotyledonous plant; monocot; rice; wheat; transgenic plant; mammalian polypeptide; antibody; expression cassette; ss.

Synthetic.

WO9966026-A2

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RRSULT 2
AAF578
ID AAF57
XX AAF58
AC AAF5
XX Endc
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                               18-JUL-2000; 2000WO-US19721.
                                                                                     25-JAN-2001.
                                                                                                                                            WO200105936-A2
                                                                                                                                                                                                  Unidentified
                                                                                                                                                                                                                                                     expression cassette;
                                                                                                                                                                                                                                                                                  Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                  Endoplasmic reticulum retention signal peptide #1 coding sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 5; 76pp; English
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DB; AAY32395.
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                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                             A new transgenic plant cell useful for producing anti-human calicivirus monoclonal antibody - \,
                                                                                                                WPI; 2003-150966/15
P-PSDB; ABJ19274.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transgenic plant; anti-human calisivirus monoclonal antibody; gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-human calisivirus monoclonal antibody related DNA SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and regenerating a population of transgenic plants from transformed cells. The present sequence is the coding sequence for an endoplasm reticulum (ER) retention signal peptide. This sequence can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a method for producing a population of transgenic plants, comprising transforming intact plant cells with minimal transgene expression cassettes by direct DNA transfer techniques.
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                                                                                                                                                                                                                                (HOKK-)
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                       acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI32073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel method of a transgenic plant, a plant body cell, a plant body, growth of a plant body, an anti-human calisivirus monoclonal antibody, and the detection of a calisivirus. This polynucleotide sequence represents DNA relating to the human calisivirus detection method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP;
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                                                                                                                                                                     invention describes novel oligonucleotide primers or peptide nucleic (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
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                                                                                 acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cyrosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for disgnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                      LysAspGluLeu
             AAGGACGAGTTA
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RESULT 7
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XX ABC271
XX ABC271
XX ABC271
XX SNP; as KW Peptid
KW Peptid
KW Centra
XX MO2001
XX MO1; i
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ABC00010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABC9989, are oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                             22-FEB-2002
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                                                                                   ABF76114;
                                                                                                                                           ABF76114 standard;
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Oligonucleotide

SEQ

IJ

NO 176111

for detecting

SNP TSC0043719

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RESULT 9
ABF7611
XX ABF761
AC ABF761
XX 22-FEB
XX Oligon
XX SNP; ss
KW peptid
KW centra
XX SNP; so
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Set of oligonucleotides, useful for diagnosis and cell typing, designed to detect single nucleotide polymorphisms and cytosin methylation status - .
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                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
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                Homo sapiens
                                               central nervous system;
                                                                                                         Oligonucleotide SEQ ID NO 176112 for detecting SNP TSC0043719.
                                                                                                                                           22-FEB-2002
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cytosine methylation; cardiovascular; primer; ss;
m; gastrointestinal; respiratory; immune; metabolic
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                                              gastrointestinal;
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                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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            07-APR-2000; 2000DE-1019173
                                          06-APR-2001; 2001WO-IB00713
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ABC00010-ABC99989, ABP00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
  Set of oligonucleotides, udesigned to detect single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic
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ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                         Claim 1; SEQ ID 229127; 29pp +
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for disgnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI22073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                          range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABE82073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                       Sequence 13
                                                                                                                                                                                             This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; peptide nucleic acid; cytosine methylation; cardiovascular; primer;
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                                                                                                                                                                                                                                                          Claim 1; SEQ ID 229129; 29pp +
                                                                                                                                                                                                                                                                                   methylation status
                                                                                                                                                                                                                                                                                               designed to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. BC00010-ABI99989, ABF00010-ABF99989, ABF0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID 229130; 29pp + Sequence Listing; German.
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ALIGNMENTS

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APPLICANT: Lenee, Philippe APPLICANT: Marden, Michael APPLICANT: Marden, Michael APPLICANT: Gruber, Veronique APPLICANT: Pagnier, Renee-Josee APPLICANT: Baudino, Sylvie APPLICANT: Baudino, Sylvie APPLICANT: Baudino, Sylvie PAPLICANT: Poyart, Claude TITLE OF INVENTION: METHOD FOR PRODUCING HAEMIN PROTEINS USING PLANT CELLS, TITLE OF INVENTION: METHOD FOR PRODUCTS CONTAINING SAME FILE REFERENCE: 8076.147USWO CURRENT APPLICATION NUMBER: US/08/983,564A CURRENT FILING DATE: 1998-06-09 PRIOR APPLICATION NUMBER: PCT/FR96/01123 PRIOR FILING DATE: 1996-07-17 NUMBER FILING DATE: 1996-07-17 NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.1

LENGTH: 12

TYPE: DNA

ORGANISM: Artificial Sequence FEATURE:

ORGANISM: Artificial Sequence Homo sapiens US-08-983-564A-24

Alignment Scores:

20.00

Matches:

Score: Smilarity: 100.00% Conservative: 0
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; FEATURE:
; OTHER INFORMATION: AntiBense Oligonucleotide
US-09-255-911-38
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US-09-255-911-38
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Query Match:
Alignment Scores: Pred. No.:
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DB:
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Best Local Similarity:
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                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF SMAD1 EXPRESSION
FILE REFERENCE: RTS-0040
CURRENT APPLICATION NUMBER: US/09/255,911
CURRENT FILING DATE: 1999-02-23
NUMBER OF SEQ ID NOS: 46
SEQ ID NO 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals,
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
                                                                                                                                                                                                                                                                                                      Sequence 38, Application US/09255911
Patent No. 6013522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 7062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00, 876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
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                                                                                  LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
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TYPE: RNA
ORGANISM: Homo sapiens
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Stinchcomb, Dan
Stinchedo, Jaime
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McSwiggen, Jim
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Indels:
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Indels:
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; TOPOLOGY:
; ANTI-SENSE:
US-09-280-805-229
                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
RESULT 5
US-09-280-805-230
                                                                                                         US-09-696-872-37 (1-4) x US-09-280-805-229 (1-20)
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US-09-280-805-229
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/280
FILING DATE: herewith
CLASSIETCATION:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 09/048,81
FILING DATE: MARCH 26, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Licata, Jane Massey
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: 159H
TREFERENCE/DOCKET NUMBER: 159H
TREFERENCE/DOCKET NUMBER: 159H
TREFERENCE/DOCKET NUMBER: 159H
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LENGTH: 20 base pairs
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OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WORDPERFECT 6.0
CURRENT APPLICATION DATA:
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ADDRESSEE: Law Offices of Jane Massey Licata
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
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APPLICANT: Graham, Brett P. Monia
                                                                                                                                                                                                                                                                                                             TYPE: Nucleic Acid
STRANDEDNESS: Single
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                                                                                                                                                                                                                                                                                 Yes
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Conservative:
Mismatches:
Indels:
Gaps:
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Matches:
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Indels:
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US-09-696-872-37 (1-4) x US-09-280-805-230 (1-20)
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Best Local Similarity:
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                                                                                                                                                                                                                    Sequence 16, Appli
Patent No. 6255105
                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: The Gov
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INFORMATION FOR SEQ ID NO:
                                                                                             APPLICANT: The Government of the United
APPLICANT: States of America as represented by the
APPLICANT: Secretary, Department of Health and Human
APPLICANT: Services; Callahan, Robert; Marchetti,
APPLICANT: Antonio; Buttitta, Fiamma; Smith, Gilbert H.
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LENGTH: 20 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Licata, Jane Massey
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-810-1515
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MEDIUM TYPE: DISKETT
                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
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APPLICATION NUMBER: 09/0.
FILING DATE: March 26, 1:
ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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APPLICANT: Graham, Brett
               TITLE OF INVENTION:
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                                                                      INVENTION:
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SEQUENCES:
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Graham, Brett P. Monia
VENTION: ANTISENSE MODULATION OF HUMAN MDM2
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20.00
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                            Nucleotide And Deduced
Amino Acid Sequences Of A New Tumor Gene,
Int6, And the Use Of Reagents Derived From
These Sequences In Diagnostic Assays,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09/048,810
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Matches:
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US-09-696-872-37 (1-4) x US-08-875-847B-16 (1-20)
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Best Local Similarity:
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                                                                                                                                                                                                                                                                      Patent No. 6342392
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS
LENGTH: 20 base pairs
                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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TITLE OF INVENTION:
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ATTORNEY/AGENT INFORMATION:
NAME: William S. Feiler
REGISTRATION NUMBER: 26,728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: (FILING DATE: 09-FEB-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 758-4800
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MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: 11
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STATE: NEW YORK
                                            CITY: NEW YORK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/875,847B FILING DATE: 09-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: UP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                     1 LysAspGluLeu 4
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10154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H: 20 base pairs nucleic acid
                           NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421792
                                                                                                                                                                                                                                                                                                     Application US/09378842
                                                         345 PARK AVENUE .
                                                                                                                                                                                         The Government of the United
States of America as represented by the
Secretary, Department of Health and Human
Services, Callahan, Robert, Marchetti,
Antonio, Buttitta, Fiamma, Smith, Gilbert H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              345 PARK AVENUE
              USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.00%
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20.00
                                                                                                     Vaccines, Immunotherapy
                                                                                                                                Nucleotide And Deduced
Amino Acid Sequences Of A New Tumor Gene,
Int6, And the Use Of Reagents Derived From
These Sequences In Diagnostic Assays,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
                                                                                                                     And Gene
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                                                                                                                  Therapy
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COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY

FLOPPY DISK

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                           FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide
US-09-702-327-66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
   US-09-696-872-37 (1-4)
                                                                                                               Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-702-327-66/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-696-872-37 (1-4) x US-09-378-842-16 (1-20)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.:
                                                                                                                                                                                        APPLICANT: C. Frank Bennett
APPLICANT: C. Frank Bennett
TITLE OF INVENTION: ANTISENSE MODULATION OF CALRETICULIN EXPRESSION
FILE REFERENCE: RTS-0097
CURRENT APPLICATION NUMBER: US/09/702,327
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 66
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 6426220
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 66, Application US/09702327 Patent No. 6426220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 421792
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/875,847

FILING DATE: 09-FEB-1996

APPLICATION NUMBER: 08/385,998

FILING DATE: 09-FEB-1995

ATTORNEY/AGENT INFORMATION:

NAME: William S. Feiler

REGISTRATION NUMBER: 26,728

REFERENCE/POCKET NUMBER: 2026-4179PCT

TELECOMYUNICATION INFORMATION:

TELEPHONE: (212) 758-4800

TELEPAX: 42/1702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
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x US-09-702-327-66 (1-20)
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                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
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APPLICANT: Lex M. Cowsett

TITLE OF INVENTION: ANTISENSE MODULATION OF CALRETICULIN EXPRESSION
FILE REFERENCE: RTS-0097
CURRENT APPLICATION NUMBER: US/09/702,327
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 67
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
COMMENT ANTISECT OF SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                         ; FEATURE: ; OTHER INFORMATION: Antisense Oligonucleotide US-09-702-327-68
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US-09-702-327-67/c
; Sequence 67, Application US/09702327
                                                         US-09-696-872-37 (1-4) x US-09-702-327-68 (1-20)
                                                                                                    Query Match:
                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                Pred. No.:
                                                                                                                                                                              Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
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                                                                                                                                                                                                                                                                             APPLICANT: C. Frank Bennett
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF CALRETICULIN EXPRESSION
FILE REFERENCE: RTS-0097
CURRENT APPLICATION NUMBER: US/09/702,327
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 68
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 68, Application US/09702327 Patent No. 6426220 GENERAL INFORMATION:
                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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                     1 LysAspGluLeu 4
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AAGGACGAGCTG 8
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Matches:
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US-08-684-672-6
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Best Local Similarity:
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                                                                                                                                                                          Sequence 6, Application US/08684672 Patent No. 5700926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (202) 289-6674
TELEX: 248516
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                     APPLICANT: KERE, Jul
APPLICANT: SCHLESSIA
APPLICANT: de la CHP
APPLICANT: SRIVASTAN
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, 1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/052,997
FILING DATE: 27-APR-1993
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                      No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DI
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Schlessinger, David
APPLICANT: de la Chapelle, Albert
TITLE OF INVENTION: ANHIDROTIC ECTODERMAL DY
TITLE OF INVENTION: AND METHOD OF DETECTING
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 289-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (204/ 207) 289-6674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: O'Shaughnessy, Brian P. REGISTRATION NUMBER: 32,747 REFERENCE/DOCKET NUMBER: 9594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: POPHAM HAIK SCHNOBRICH & KAUFMAN, LTD STREET: 1225 Eye Street N.W., Suite 1000 CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
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FORMALL.

JETE KERE, Juha

NT: KERE, Juha

NT: SCHLESSINGER, David

NT: SCHLESSINGER, Albert

ANT: SRIVASTAVA, Anand Kumar

OF INVENTION: MOLECULAR CLONING OF THE ANHIDROTIC

THYPENTION: ECTODERMAL DYSPLASIA GENE
                                                                                                                                                                                                                                                                                     1 LysAspGluLeu 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
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20.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                  Indels:
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RESULT 13
US-09-191-852-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
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Sequence 5, Apr-
No. 6194560
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/684,672
FILING DATE: 22-UTL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (703) 836-2021 INFORMATION FOR SEQ ID NO:
ZIP: 77010

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/191,852
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: O'Shaughnessy, Brian P.
REGISTRATION NUMBER: 32,747
REFERENCE/DOCKET NUMBER: 030956-002
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
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CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                   STREET: 1301 N
CITY: Houston
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STREET: P.O. Box 1404
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                                                                                                                                                                                                                                                                                                                                                                                                         1301 McKinney,
                                                                                                                                                                                                                                                                                                           USA
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Indels:
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Matches:
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Percent Similarity:
Best Local Similarity:
Query Match:
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SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 315,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                        COMPUTER KEALANDLA COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
**DOLICATION NUMBER: US/07/974,409C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Akitaya, Tatsuo
APPLICANT: Mitsuhashi, Masato
APPLICANT: Cooper, Allan
TITLE OF INVENTION: METHOD AND REAGENT
TITLE OF INVENTION: FOR MEASURING MESSENGER RNA
                                                            NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: HITACHI.006CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
                                                                                                                                                                    APPLICATION NUMBER: US/07
FILING DATE: 12-NOV-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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No.:
                                SEQUENCE CHARACTERISTICS:
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ADDRESSEE: Knobbe, Martens, Olson, and Bear
STREET: 620 Newport Center Dr. Sixteenth Floor
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TELEPHONE: 713-651-5151
TELEFAX: 713-651-5246
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                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Newport Beach
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REFERENCE/DOCKET NUMBER: P01590US1
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FILING DATE: 24-OCT-1995
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              ENGTH:
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nucleic acid
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Matches:
Conservative:
Mismatches:
Indels:
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                                                            Score:
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US-07-974-409C-316
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US-07-974-409C-316/c
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Best Local Similarity:
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Patent No. (
                                                                                                                                                                                                                        TELEPHONE: 714-760-040
TELEPAX: 714-760-9502
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 22
                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: HITA
TELECOMPUNICATION INFORMATION:
TELEPHONE: 714-760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                   MOLECULE TYPE:
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/974,409C
FILING DATE: 12-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson, and Bear
STREET: 620 Newport Center Dr. Sixteenth Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Mitsuhashi, Masato
APPLICANT: Cooper, Allan
TITLE OF INVENTION: METHOD AND REAGENT
TITLE OF INVENTION: FOR MEASURING MESSENGER RNA
NUMBER OF SEQUENCES: 457
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HYPOTHETICAL: NO
ANTI-SENSE: NO
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                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: doub
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TOPOLOGY: linear
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Gaps:
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Matches:
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Gaps:
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US-09-696-872-37 (1-4) x US-07-974-409C-316 (1-22)

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Search completed: August 26, 2003, 19:22:50 Job time : 4.15044 secs

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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                                              Score
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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Ygapop 10.0,
Fgapop 6.0,
Delop 6.0,
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Match Length DB
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1 KDEL 4
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/cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/USO9A_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/USO9A_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/USO9C_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/USO9C_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/USO0A_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/USOOA_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/USOOA_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/PC7_NEW_PUB.seq:*
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                                       Description
Sequence 1, Appli
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Patent No. US20020078472A1
GENERAL INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/333,527
FILING DATE: Concurrently Herewith
CLASSIFICATION:
                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSE: Fulbright & Jaworski L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Paul CH
TITLE OF INVENTION:
  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                            STATE: New COUNTRY: US ZIP: 10103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                       Concurrently Herewith
                                                                                                                                                                                                                                                                                                                                                                               CHRISTOU; Eva STROGER; Rainer FISCHER; Carmen MARTIN-VAQUERO; Stefa
DN: METHODS AND MEANS FOR EXPRESSION OF MAMMALIAN POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.25
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4 US-10-287-919-1514

4 US-10-287-919-1515

4 US-10-287-919-2042

4 US-10-287-919-2043

4 US-10-287-919-2043

4 US-10-287-919-2043

1 US-09-780-533A-652

1 US-09-780-533A-653

1 US-09-780-533A-1501

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1 US-09-780-33A-1501

1 US-09-780-33A-1501
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US-09-791-406-67

US-09-791-406-68

US-09-858-152A-16

US-09-868-778A-11

US-09-866-778A-11

US-09-866-778A-11
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US-10-079-167-3
US-10-286-628-7
US-09-263-959-1077
US-09-263-959-1077
US-10-215-112-2977
US-10-298-263B-1698
US-10-098-263B-10867
US-10-098-263B-10867
US-10-098-263B-17233
US-10-098-263B-17234
US-10-098-263B-17234
US-10-098-263B-17234
US-10-098-263B-17234
US-10-098-263B-17234
US-10-098-263B-50278
US-10-098-263B-50278
US-10-098-263B-50279
US-10-098-263B-50279
US-10-098-263B-50279
US-10-098-263B-766097
US-10-098-263B-76429
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Sequence 1, Appli
Sequence 1515, Ap
Sequence 2042, Ap
Sequence 2043, Ap
Sequence 652, App
Sequence 653, App
Sequence 654, App
Sequence 230, App
Sequence 270, App
Sequence 66, Appl
Sequence 67, Appl
Sequence 10, Appl
Sequence 107, Appl
Sequence 107, Appl
Sequence 1071, Appl
Sequence 10722, A
Sequence 10931, A
Sequence 10867, A
Sequence 17234, A
Sequence 17333, A
Sequence 1733, A
Sequence 17417, A
Sequence 53659, A
Sequence 66666, A
Sequence 70671, A
Sequence 71415, A
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APPLICANT: Baudino, Sylvie
APPLICANT: Baudino, Sylvie
APPLICANT: Baudino, Sylvie
APPLICANT: Poyart, Claude
ITILE OF INVENTION: METHOD FOR PRODUCING HAEMIN PROTEINS USING PLANT
ITITLE OF INVENTION: CELLS,
ITITLE OF INVENTION: RESULTING PROTEINS AND PRODUCTS CONTAINING SAME
FILE REFERENCE: 8076.147USMO
CURRENT APPLICATION NUMBER: US/10/085,853
CURRENT FILING DATE: 2001-10-18
PRIOR APPLICATION NUMBER: 08/983,564
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: PCT/FR96/01123
PRIOR FILING DATE: 1998-07-17
PRIOR APPLICATION NUMBER: 95/08615
PRIOR FILING DATE: 1995-07-17
UNDBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN Ver. 2.1
   Query Match:
Da:
                                Percent Similarity:
Best Local Similarity:
                                                                                                                           ; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
US-10-085-853-24
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                                                                              Pred. No.:
                                                                                                 Alignment Scores:
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DB:
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Best Local Similarity:
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                                                                                                                                                                                                                         SOFTWARE: PA
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APPLICANT:
APPLICANT:
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APPLICANT: Dieryc
APPLICANT: Lenee,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: June 15, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Mary Anne Schofield
REGISTRATION NUMBER: 36,669
REFERENCE/DOCKET NUMBER: KL/JIC 202.1
TELECOMMUNICATION INFORMATION:
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Gruber, Veronique
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Matches:
Conservative:
Mismatches:
Indels:
                                              Length:
Matches:
Conservative:
Indels:
Gaps:
                                Mismatches:
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RESULT 4
US-10-287-919-1514/c
; Sequence 1514, Application US/10287919
; Publication No. US20030085830A1
                                                                                                                                                                              US-09-696-872-37 (1-4) x US-10-127-427-1 (1-12)
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                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
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US-10-127-427-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Mary Anne Schofield
REGISTRATION NUMBER: 36,669
REFERENCE/DOCKET NUMBER: KL/JIC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/089,322
FILING DATE: June 15, 1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/333,527
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: METHODS AND MEANS FOR EXPRESSION OF MAMMALIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Paul CHRISTOU; Eva STROGER; Rainer FISCHER; Carmen MARTIN-VAQUERO; Stefan SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AAAGATGAGCTA 12
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OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
                                                                                                     AAAGATGAGCTC 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/10/127,427
FILING DATE: 23-Apr-2002
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                              IOPOLOGY:
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Matches:
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                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: (809601)...(809615); OTHER INFORMATION: Chromosome US-10-287-919-1515
                                                                                                  RESULT 6
US-10-287-919-2042
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; OTHER INFORMATION: Chromosome = 1
US-10-287-919-1514
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Pred. No.:
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Best Local Similarity:
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GENERAL INFORMATION:

APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.

TITLE OF INVENTION: Methanococcus jannaschii complete genor

FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333

CURRENT APPLICATION NUMBER: US/10/287,919

CURRENT FILING DATE: 2002-11-05

NUMBER OF SEQ ID NOS: 2706

SOFTWARE: Proprietary
Sequence 2042, Application US/10287919
Publication No. US20030085830A1
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
APPLICANT: Modern Methanococcus jannaschii complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Methanococcus jannaschii complete genome.

FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333

CURRENT APPLICATION NUMBER: US/10/287,919

CURRENT FILING DATE: 2002-11-05

NUMBER OF SEQ ID NOS: 2706

SOFTWARE: Proprietary

SEQ ID NO 1514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 1515
LENGTH: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Methanococcus jannaschii complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Methanococcus jannaschii complete
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Matches:
Conservative:
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Matches:
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Query Match:
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Best Local Similarity:
                                                                       US-09-780-533A-652/c
                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                    US-09-696-872-37 (1-4) x US-10-287-919-2043 (1-15)
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Publication No. US20030085830A1

GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants,
TITLE OF INVENTION: Methanococcus jannaschii complete
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/287,919
CURRENT FILING DATE: 2002-11-05
NUMBER OF GEO TO TO TO TO TO THE COMPLETE TO THE COM
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SOFTWARE: Proprietary
SEQ ID NO 2043
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Sequence 652, Application US/09780533A Publication No. US20030060611A1
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CURRENT FILING DATE: 2002-11-05
NUMBER OF SEQ ID NOS: 2706
SOFTWARE: Proprietary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Methanococcus jannaschii complete genome
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OTHER INFORMATION: Chromosome =
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GENERAL INFORMATION:

APPLICANT:
APPLICANT:

APPLICANT:

APPLICANT: Ribozyme Pharmaceuticals, Inc. APPLICANT: Blatt, Larry

McSwiggen, Jim Chowrira, Bharat Haeberli,

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                  US-09-780-533A-654/c
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                                                                                                                                                                                                              US-09-696-872-37 (1-4) x US-09-780-533A-653 (1-17)
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US-09-780-533A-653
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                                 Sequence 654, Application US/09780533A Publication No. US20030060611A1 GENERAL INFORMATION:
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LENGTH: 17
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LENGTH: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: McSwiggen, Jim
APPLICANT: Chowrira, Bharat
APPLICANT: Haeberli, Pete
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
FILE REFERENCE: MBHB00,878-A (400/011)
CURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,797
PRIOR PILING DATE: 2000-02-11
NUMBER OF SEO ID NOS: 6679
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEO ID NOS: 6679
APPLICANT: Ribozyme Pharmaceuticals, Inc. APPLICANT: Blatt, Larry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ribozyme Pharmaceuticals, Inc. APPLICANT: Blatt, Larry APPLICANT: McSwiggen, Jim
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PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 6679
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CURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT FILING DATE: 2001-02-09
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RESULT 12
US-09-969-373-3751
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APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: Chowrira, Bharat
APPLICANT: Haeberli, Pete
TITIE OF INVENTION: Method and Reagent for th
FILE REFERENCE: MBHB00, 878-A (400/011)
CURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT APPLICATION NUMBER: US 60/181,797
PRIOR APPLICATION UMBER: US 60/181,797
PRIOR APPLICATION UMBER: US 60/181,797
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US-09-780-533A-1501/c
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Best Local Similarity:
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Pred. No.:
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CURRENT APPLICATION: Method and Reagent for the Inhibition of NOGO Gene CURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,797
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 6679
SOPTWARE: PatentIn version 3.0
SEQ ID NO 654
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 1501
LENCTH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1501, Application US/09780533A Publication No. US20030060611A1
                                                                                                                                                                                                                                                                                                              TYPE: RNA
ORGANISM: Homo sapiens
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TYPE: RNA
ORGANISM: Homo sapiens
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Sequence 3751, Application US/09969373 Patent No. US20020133852A1

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RESULT 13
US-09-752-983-229
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Best Local Similarity:
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; ORGANISM: Glycine max
US-09-969-373-3751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
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PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 4593
SEQ ID NO 3751
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Patent No. US20010016575A1
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TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping FILE REFERENCE: 38-10(52679)A
CURRENT APPLICATION NUMBER: US/09/969,373
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US 09/754,853
PRIOR FILING DATE: 2001-01-05
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 09/760,427
PRIOR APPLICATION NUMBER: US 09/760,427
PRIOR FILING DATE: 2001-01-13
TELEFAX: 609-810-1454
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Hauge, 1
                                                    NAME: Licata, Jane Massey
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0346
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-810-1515
                                                                                                                                                     APPLICATION NUMBER: 09/28
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                       SOFTWARE: WORDPERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/752,983
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MEDIUM TYPE: DISKETT
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APPLICANT: Graham, Brett P. Monia
TITLE OF INVENTION: ANTISENSE MODULATION OF HUMAN MDM2
TITLE OF INVENTION: EXPRESSION
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                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC
OPERATING SYSTEM: WINDOWS 95
                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                         FILING DATE: 02-Jan-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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66 East Main Street
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                                                                                                                                                                                                                                                                                                                                                                          DISKETTE,
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Indels:
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; TYPE: Nucleic Acid
STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
US-09-752-983-229
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US-09-752-983-230
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Loren J. Miraglia, Pame APPLICANT: Graham, Brett P. Monia APPLICANT: Graham, Brett P. Monia
                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/280,
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Licata, Jane Massey
REGISTRATION NUMBER: 32,25:
                                                                                                                                                                                                                        TELEFAX: 609-810-1454
INFORMATION FOR SEQ ID NO:
                                                                                                                                 TOPOLOGY:
ANTI-SENSE:
                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: IS TELECOMMUNICATION INFORMATION: TELEPHONE: 609-810-1515
                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: WORDPERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09,
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MEDIUM TYPE: DISKETT
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                       LENGTH: 20 base pairs
TYPE: Nucleic Acid
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CITY: Marlton
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OPERATING SYSTEM: WINDOWS 95
                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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                                                                                                                                    Yes
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                                                       Length:
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Indels:
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Sequence 66, Application US/09791406

Patent No. US20020147165A1

GENERAL INFORMATION:

APPLICANT: C. Frank Bennett

APPLICANT: Robert Rothlein

APPLICANT: Takashi Kei Kishimoto

APPLICANT: Lex M. Cowsert

ITITLE OF INVENTION: ANTISENSE MODULATION OF CALRETICULIN EXPRESSION

FILE REFERENCE: RTS-0097

CURRENT APPLICATION NUMBER: US/09/791,406

CURRENT FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 89

SEQ ID NO 66

LENGTH: 20

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide

US-09-791-406-66
                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Search completed: August 26, 2003, 21:02:50 Job time: 12.5044 secs
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                                                                                                                           US-09-696-872-37 (1-4) x US-09-791-406-66 (1-20)
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US-09-791-406-66/c
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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-Q=/cgn2_1/USPTO_spool/USO9986872/runat_26082003_151137_3236/app_query.fasta_1.462
-Q=/cgn2_1/USPTO_spool/USO9986872/runat_26082003_151137_3236/app_query.fasta_1.462
-DB=EST -OFMT=fastap -SUFFIX=rst -MINNATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR MAX=100 -THR MIN-0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pct -NORM=ext -HEAPSIZE=50 -MINLEN=0 -MAXIEN=2000000000
-USER=US09696872_@CGN_1_1_3596_@runat_26082003_151137_3236 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQTERY -NEG_SCORES=0 -MATIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MARN_TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum DB seq length: 200000000
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Perfect score:
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Ygapop 10.0 , Y
Fgapop 6.0 , F
Delop 6.0 , I
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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

REFERENCE	SOURCE ORGANISM	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	AU254198	RESULT 1
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 25)	Mus musculus (house mouse) Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	EST.	AU254198.1 GI:20315754	AU254198	BED0000932 3', mRNA sequence.	AU254198 3'-directed mouse cDNA library Mus musculus cDNA clone	AU254198 25 bp mRNA linear EST 25-APR-2002		

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BASE COUNT
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AUTHORS
TITLE
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TITLE
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COMMENT
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MUSGS00978 Mouse 3'-direc mb0732 3', mRNA sequence. D19573
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Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5581
                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 32)
Kawamoto,S., Okubo,K., Yoshii,J., Katsuki,M. and Matsubara,K.
Analysis of gene expression in mouse embryogenesis by 3'-dire
                                                                                                                                                                                                                         3-1 Yamada-oka,
                                                                                                                                                                                                                                      Osaka University
                                                                                                                                                                                                                                                                              Contact: Kawamoto, S., Okubo, K., Yoshii, J., Katsuki, M.
                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus domesticus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: kkato@bs.aist-nara.ac.jp,
URL:http://love2.aist-nara.ac.jp/BED/index.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Generation of expressed sequence tags from mouse brain Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus domesticus (western European house mouse)
                                                                                                                                                                                                                                                    institute for Cellular and Molecular Biology
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/mol type="mRNA"
/db xref="teaxon:10090"
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/tissue type="brain"
/clone_Tib="3'-directed musculus"
a 5 5
                                                                     /db_xref="taxon:10092"
/clone="mb0732"
/tissue_type="decidual tissue
/clone_Tib="Mouse_3'-directed"
/ d c 5 g 9 t
                                                                                                                                                                                                        a-oka, Suita, Osaka 565, Japan.
Location/Qualifiers
                                                                                                                                               mol_type="mRNA"
|strain="C57BL/6J"
                                                                                                                                                                          organism="Mus musculus
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Silurana tropicalis (western clawed frog)
Silurana tropicalis
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Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, J
Tel: 81-743-72-5581
                                                                                  AL801834
AL801834.1 GI:21588202
                                                                                                                         AL801834 XGC-neurula Silurana
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AU254805 3'-directed mouse CDNA
BED0003418 3', mRNA sequence.
AU254805
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                             mRNA sequence.
                                                                                                                                         AL801834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: kkato@bs.aist-nara.ac.jp,
URL:http://love2.aist-nara.ac.jp/BED/index.html.
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Kato, K. and Matoba, R.
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Kenopodinae; Silurana
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/tissue_type="brain"
/clone_Tib="3'-directed mouse cDNA library"
/s 4 g 9 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Mus musculus"
/mol_type="mRNA"
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TNeu097103 5',
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                                                                                                                                                                                                                          Williams, S.A., Lizotte-Waniewski, M., Laney, S., Wenhong, L., Hillier, L., Allen, M., Bowles, L., Geisel, S., Jost, S., Kucaba, T., Martin, J., Steptoe, M., Theising, B., White, Y., Wylie, T., Chappell, J., Person, B., Gibbons, M., Harvey, N., Pape, D., Chamberlain, A., Morales, R., Schurk, R., Ritter, E., Kohn, S., Underwood, K. and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Al130296 APP MRNA linear EST 26-MAR-19 SWOVL52AN08G12 Onchocerca volvulus infective larva CDNA (SAW94WL-OvL3) Onchocerca volvulus cDNA clone onch276 5' similar TR:001657 001657 FRUCTOSE-BISPHOSPHATE ALDOLASE ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST
TROPICALIS_SEQUENCE_ID: TNeu09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Taylor,R., Ashurst,J.L., Croning,M.D.R., Zorn,A.M. Sanger Xenopus tropicalis EST project 2002 Unpublished
                                                                                Smith College Department of Biological Department of Biological Sciences, Cla. College, Northampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                                                                                           Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing primer: P1CSP6
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                                                                                                                                                Molecular Parasitology
                                                                                                                                                                    Contact: Steven A. Williams
                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                           Molecular Parasitology OvL3
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                                                                lege, Northampton, MA, 4135853826
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library was constructed by Wenhong Lu.
                                             4135853786
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                       genome@smith.edu
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//clone_lib="XGC-neurula"
/note="YGctor: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
/note="Vector: pCS107; Site_1: EcoRI, Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from neurula.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end."

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/db_xref="taxon:8364"
/clone="TNeu097103"
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  The library is available
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AI208498
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                     CONA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares,
                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 51)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                               Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/strain="Sierra Leone"
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                                This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of At1g20210 and 300 bases of the 5' end of At1g20210. Class: TDNA tagged.
                                                                                                                                                                        Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosid; eurosids II; Brassicales; Brassicacea; Arabidopsis.

1 (bases 1 to 51)
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                                                                                                                                                                                                                                                                                        Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,i, Zinmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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                                                                                                                 Email: ecker@salk.edu
                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                        Arabidopsis Genome
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858 558 6379
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                  Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
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AV555282/c
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                                                                                                                                                                                                                                                                                                                                                   The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
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1 (bases 1 to 52)

Asamizu, E., Nakamura; Y., Sato, S. and Tabata; S.
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AV555282 Arabidopsis thaliana green siliques Columbia Arabidopsis
thaliana cDNA clone SQ010f02F 3', mRNA sequence.
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/clone="$ALK 137492.43.00.x"
/clone=lib="Ārabidopsis thaliana TDNA insertion lines"
/clone=lib="Arabidopsis thaliana lines //clone="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

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                                                                                                                                                         tissue_type="green siliques"
/clone_lib="Arabidopsis thaliana green siliques Columbia"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
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/mol_type="mRNA"
/strain="Columbia"
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/strain="Columbia 0"
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Department of Biological Sciences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class: transposon-tagged.
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Possible ligation site of ends cut
Reverse complemented post-ligation
Plate: 1007066 column: 35
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                                                                                                                                                                       /clone_lib="1007 - RescueMu Grid H"
/clone="Corgan: leaf; Vector: RescueMu (engineered from /note="Corgan: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site_2: BgIII;
RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb iastate.edu' and follow the links for 'RescueMu.' Grid H was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BgIII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
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BH620522 (1-52)
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                                          RESULT 11
AU259239/c
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US-09-696-872-37 (1-4) x AA837889 (1-53)
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56 bp mRNA linear EST 25-APR-;
AU259239 3'-directed mouse cDNA library Mus musculus cDNA clone
BED0014799 3', mRNA sequence.
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cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consorthum/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 857 Std Error: 0.00
Seg primer: -40ml3 fwd. ET from Amersham
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone_lib="NCI_CGAP_Pr25"
/note="Torgan: prostate; Vector: Bluescript SK-; Site_1:
/note="Torgan: prostate; Vector: Bluescript SK-; Site_1:
/note="Torgan: prostate; Vector: Bluescript SK-; Site_1:
/note="Torgan: prostate epithelial cell line (HPV oligo dT. Normal prostate epithelial cell line (HPV olimortalized). 5' adaptor sequence: 5' GAATTCGGCACGAG 3'
/ adaptor sequence: 5' CTGGAGTTTTTTTTTTTTTTTTTT 3'
/ Average insert size: 1.1 kb."

a 12 c 8 g 11 t 1 others
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/db_xref="taxon:9606"
/clone="iMAGE:1411008"
/tissue_type="epithelium (cell line)"
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RESULT 12
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                                                                             Unpubliand Joseph R. Ecker
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
The Salk Institute for Biological CA 92037, USA
                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 59)
1 (bases, J. M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J. R.

A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                BZ769592 59 bp DNA linear GSS 13-MAR-2003 SALK 142419.31.10.n Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK 142419.31.10.n, genomic
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                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                        Email: ecker@salk.edu
                                                          10010 N. Torrey Pines Road,
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                       Unpublished
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URL:http://love2.aist_nara.ac.jp/BED/index.html
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Kato, K. and Matoba, R.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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 single pass sequence recovered from the left
his sequence lies within an annotated exon of
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/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="BED0014799"
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BJ080266.1 GI:17573878
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopus laevis (African clawed frog) Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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/clone="Elb="Exabldopsis thaliana TDNA insertion lines"
/clone="EPCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
a 9 c 14 g 19 t
                                                                            /dev_stage="stage 25"
/clone_lib="NIBB Mochii normalized Xenopus
library"
9 c 14 g 13 t 3 others
                                                                                                                                                                    /organism="Xenopus laevis"
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/clone="XL075a15"
                                                                                                                                                    tissue_type="whole embryo"
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/db_xref="taxon:3702"
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The Berkeley Drosophila Genome Project Gene Disruption Project
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University of California, Berkeley
LSA Building, Berkeley, CA 94720-3200,
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Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: gerry@fruitfly.berkeley.edu
Sequence recovery method was inverse PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Gerald Rubin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
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Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
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eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
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/clone_lib="Arabidopsis thaliana flower buds Columbia"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
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/mol_type="mRMA"

/strain="Columbia"

/db_xref="taxon:3702"

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E 1 (bases 1 to 372)
S Rothman,J.E., Mayhew,M. and Hoe,M.H.
KDEL receptor inhibitors
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/organism="unknown"
a 102 c 122 g
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96 c 106 g
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                                                                                                                                         72.9%;
83.1%;
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                                                                                                                               0;
                                                                                                                              Score 271.2; DB 6;
Pred. No. 2.1e-46;
0; Mismatches 63;
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Pred. No. 2.3e-67;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                       372 bp
US 6160088
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AR121630
LOCUS
DEFINITION
RESULT 4
AR121627
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Unknown.
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Sequence 28
AR121630
AR121630.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 372)
Rothman, J.E., Mayhew, M. and Hoe, M.H.
KDEL receptor inhibitors
Patent: US 6160088-A 28 12-DEC-2000;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                       ATGCATCTCGAG
                                                                                                GAACCGGAAGGTACCGGATCATCAGAAAAAGATGAGTTGTAGGCGGCGCCGCAGAATTCCAT
                                                                                                                                            CAGCCGCAGCCGAAACCGCAGCCGCAGCCGCAGCCGCAGCCGAAACCGGCAGCCGAAACCG
                                                                                                                                                                                    CAGGTCAGGGAGATCACGTTCCTGAAAAAACACGGGGGATGGAGGGATGTGACGCGTGCGGGCCG
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                                         ATGCATCTCGAG
                                                                                    GAACCGGAAGGTACCGGATCATCAGAAAAAGATGAGTTGTAGGCGGCCGCAGAATTCCAT
                                                                                                                               CAGCCGCAGCCGAAACCGCAGCCGCAGCCGCAGCCGAAACCGCAGCCGAAACCG
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105 c 109 g
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82.0%;
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Pred. No. 4.5e-45;
0; Mismatches 67;
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US 6160088
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BASE COUNT
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DEFINITION
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AUTHORS
TITLE
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FEATURES
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AR121626
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Sequence 20
AR121626
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Sequence 22
AR121627
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Rothman, J.E., Mayhew, M. and Hoe, M.H.
KDEL receptor inhibitors
RDEL receptor inhibitors
Patent: US 6160088-A 22 12-DEC-2000;
                                                                                                                                   1 (bases 1 to 369)
Rothman, J.E., Mayhew, M. and Hoe, M.H.
KDEL receptor inhibitors
Patent: US 6160088-A 20 12-DEC-2000;
                                                                                                                                                                                             Unknown
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AAGGATCCAGCCTGGGTGGAGACTGTTGTTCAGACCTGGGCCCGCAGATGCTTCGGGAAC 130
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                                  52.2%;
ilarity 77.5%;
Conservative
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                                                                                      /organism="unknown"
103 c 120 g
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94 c 121 g
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                                 Score 194; DB 6; L
Pred. No. 2.4e-30;
0; Mismatches 68;
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Pred. No. 5.2e-32;
0; Mismatches 63
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Sequence
AR121623
                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 387)
Rothman, J.E., Mayhew, M. and Hoe, M.H. RDEL receptor inhibitors
Patent: US 616088-A 14 12-DEC-2000;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unknown
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                                                       TCGAG 372
                                                                                                                         AGCCGAAACCGCAGCCGCAGCCGCAGCCGCAGCCGAAACCGCAGCCGAAACCGGAACCGG
                                                                                                                                      AGCCGAAACCGCAGCCGCAGCCGCAGCCGCAGCCGAAACCGGCAGCCGAAACCGGAACCGG
                                                                                                                                                                                   TGGAGTGTGACGCGTGCG------
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                                                                               AAGGTACCGGATCATCAGAAAAAGATGAGTTGTAGGCGGCCGCAGAATTCCATATGCATC
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                                                                                                                                                                                                                                                                                                       Score 193.4; DB 6;
Pred. No. 3.2e-30;
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c US /
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AR121632
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Sequence 16
AR121624
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Rothman, J.E., Mayhew, M. and Hoe, M.H.
KDEL receptor inhibitors
Patent: US 6160088-A 16 12-DEC-2000;
Location/Qualifiers
1. .387
                                                                          1 (bases 1 to 444)
Rothman, J.E., Mayhew, M. and Hoe, M.H.
KDEL receptor inhibitors
Patent: US 6160088-A 3512-DEC-2000;
                                                                                                                                                                               Sequence 35
AR121632
                                                                                                                        Unclassified
                                                                                                                                     Unknown
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                                                                                                                                                                                                                                                            GATGAGTTGTAGGCGGCCGCAGAATTCCATATGCATCTCGAG
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                                                                                                                                                                                                                                                                                                                   CAGCCGCAGCCGAAACCGCAGCCGAAACCGGAAGCCGGAAGGTACCGGATCATCAGAAAAA
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                                                                 Location/Qualifiers
                                /organism="unknown"
122 c 134 g
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107 c 126 g
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Pred. No. 6.2e-30;
0; Mismatches 50
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Sequence
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Rothman, J.E., Mayhew, M. and Hoe, M.H.
KDEL receptor inhibitors
Patent: US 6160088-A 18 12-DEC-2000;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                      Unknown
                                                                                                                                                                                                                                              h 47.7%;
Similarity 73.4%;
73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           Unclassified
                                                                                                                                                                                                                                                                                                                                                                                                                   Unknown
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                                                                                   CAGGTCAGGGAGATCACGTTCCTGAAAAACACGGTGATGGAGTGTGACGCGTGCGGGCCG
                                                                                                                                                                   GCTGCCAAAAAAGGATCCAGCCTGGGTGGAGACTGTTGTTCAGACCTGGGCCCGCAGATG
                                                                                                                                                                                                                  AAGCTTACCATGGGAAGGTACATGATTTTAGGCTTGCTCGCCCCTTGCGGCAGTCTGCAGC
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                                    CAGCCGCAGCCGAAACCGCAGCCGCAGCCGCAGCCGCAGCCGAAACCGCAGCCGAAACCG
                                                                 CAGGTGAAGGAAATGTCACTCATCCGGAACACCATCATGGAGTGTCAGGTGTGCGGTCCG
                                                                                                                                  CTTCGGGAAACTGCAGGAAACCAACGCGGGGCGCTGCAGGACGTGCGGGACTGCGGCAG
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 GAACCGGAAGGTACCGGATCATCAGAAAAAGATGAGTTGTAGGCGGCCGCAGAATTCCAT
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100 c 114 g
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                                                                                                             CTCACCCTCTTCAACCAGATCCTAGTGGAGCTTCGGGACGACATCCGAGAC
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                                                                                                                                                                                                                                              Score 177.6; DB 6
Pred. No. 6.2e-27;
0; Mismatches 84
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Sequence 26 from patent
AR121629
                                                                                                 Homo sapiens comp
complete cds.
AB086984
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Rothman, J.E., Mayhew, M. and Hoe, M.H. ROEL receptor inhibitors

Patent: US 6160088-A 26 12-DEC-2000;

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unknown
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           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                         Homo sapiens
                                                      Homo sapiens (human)
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Pred. No. 1.6e-22;
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                                                                                                                          2274 bp mRNA linear PRI for cartilage oligomeric matrix
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human comp cDNA with Unpublished
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Hashimoto, Y. and Mori, H.
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                                                   EGF-like repeats"
/replace="g"
670
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/note="SNIPs of # 4
EGF-like repeats"
/replace="c"
EGF-like repeats"
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DPGILAVITARNGVD PEGTEHVNI TVIDDI VAGET I FGY ODSSE FVVNMIKOMEQIT WQA
NPFRAVAEPGI OLKAVKSYGOFGOLENAL MHTGDTESQVRILLI MKD PRIVOKINKKKY
RWFLQHR PQVGY I RVR FYEGPELVADSNVVLD TTMRGGRLGVFCFSQENI I WANLRYR
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SDQKDSDGDGIGDACDNCPQKSNPDQADVDHDFVGDACDSDQDQDGDGHQDSRDNCPT
VPNSAQEDSDHDGQGDACDDDDDNDGVPDSRDNCRLVPNPGQEDADRDGVGDVCQDDF
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669
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EGF-like repeats"
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replace="+"
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/note="SNIPs of # 1,
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SGCQRGAQRFCPDGSPSECHEHADCVLERDGSRSCVCRVGWAGNGILCGRDTDLDGFP
DEKLRCPEPQCRKDNCVTVPNSGQEDVDRDGIGDACDPDADGDGVPNEKDNCPLVRNP
                                                                                                                                                                                                                                                                                                                                                                    /note="SNIPs of #formation domain"
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LQDVRDMLRQQVREITFLKNTVMECDACGMQQSVRTGLPSVRPLLHCAPGFCFPGVAC
IQTESGGRCGPCPAGFTGNGSHCTDVNECNAHPCFPRVRCINTSPGFRCEACPPGYSG
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/product="cartilage oligomeric matrix protein"
/protein id="BAC53888.1"
/db_xref="GI:27530066"
                            gene="comp"
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xref="taxon:9606"
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Best Local Similarity
Matches 145; Conserva
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Sequence 441 from Patent WOO194629.
AX329932
AX329932.1 GI:18102910
                                                                                                                   Patent: WO 0194629-A 441 13-DEC-2001;
Avalon Pharmaceuticals (US)
Location/Qualifiers
                                                                                                                                                                 Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z.
Cancer gene determination and therapeutic screening using signature
                                                                                                                                              gene sets
Patent: W
                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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    38.3%;
llarity 97.3%;
Conservative
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/note="SNIPs of # 10, 11 are localized in a stuffed
sequence between the EGF-like repeats and the TSP ty
repeats"
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/note="SNIP8 of #
EGF-like repeats"
                                                          /mol_type="genomic DN
/db_xref="taxon:9606"
758 c 809 g
                                                                                   /organism="Homo sapiens"
/mol_type="genomic DNA"
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/note="SNIPs of #
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/note="SNIPs of #
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  Score 142.6; DB 6;
Pred. No. 9.9e-20;
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Pred. No. 1e-19;
0; Mismatches 4;
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Sequence 1426 from Patent WOC
AX330917
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Avalon Pharmaceuticals (US)
Location/Qualifiers
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AX330698
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Homo sapiens
                        Young, P.E., Augustus, M., Carter, K.C., Horrigan, S., Soppet, D.R. and Weaver, Z.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
758 c 809 g 36
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gene sets
Patent: WO 0194629-A 1426 13-DEC-2001;
                                                           Horrigan, S., Soppet, D.R. and Weaver, Z. Cancer gene determination and therapeutic
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 9.9e-20;
0; Mismatches 4;
                                                                                                                  Ebner, R.,
                                                                 screening using signature
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L32137
L32137.1
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Newton,G., Weremowicz,S., Morton,C.C., Copeland,N.G., Gilbert,D. Jenkins,N.A. and Lawler,J.
Characterization of human and mouse cartilage oligomeric matrix
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                               Original source text: Homo sapiens cartilage cDNA to mRNA.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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germline oligomeric matrix protein (COMP) mRNA,
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VPNSAQEDSDHDGQGDACDDDDDDDGVPDSRDNCRLVPNPGQEDADRDGVGDVCQDDF
DADKVVDKIDVCPENAEVTLTDFRAFQTVVLDPEGDAQIDPNWVVLNQGREIVQTMNS
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/db_xref="taxon:9606"
758 c 809 g
                                                                                                                                                       product="matrix protein"
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/db_xref="GI:602450"
                                                                                                                                                                                                   /gene="COMP"
/gene="Comp"
/standard_name="cartilage oligomeric matrix protein"
/note="putative"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"

mol_type="mRNA"

db_xref="taxon:9606"
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cell_type="chondrocyte"
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VA, complete cds.
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BASE COUNT
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Search completed: August 26,
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/rpt_tamily="thrombospondin type 2"
/rpt_type=tandem
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NPFRAVAEPGIQLKAVKSSTGPGEQLKNALMHTGDTESQVRLLMKDPRAVGWKDKKSY
RWFLCHRPQVGYIRVEFYEGPELVADSNVVLDTTMRGGRLGVFCFSQENIIMANLRYR
CNDTIPEDYETHQLRQA"
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2439
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/rpt family="thrombospondin type 3"
/rpt type=tandem
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Listing first 45 summaries
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1: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.

2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.

3: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.

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5: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1984.

6: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1985.
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ALIGNMENTS

cDNA downregulated	ACA03912	25	3747	14.2	53	٠.
Human cDNA differe	ABK84787	24	1412	14.2	53	-
Human cancer assoc	AAC78047	21	1082	14.2	53	
Human lung tumour	ABL49239	24	521	14.2		
	ABQ92425	24	521	14.2		_
	AAC66020	21	521	14.2		•
	ABL03152	23	5178	14.4	53.4	·
	ABL03153	23	98	14.4	53.4	w
O	AAC84677	22	5120	14.4	53.6	7
Trinucleotide repe	ABK10240	21	403	14.4	53.6	٠,
Spinocerebellar at	AAX89891	20	397	14.5	Ψ	٧.
Exons D, C, B and	AAA59241	21	1472	4.	55	-
oRI fi	AAA59240	21	1159	٠	55	w
Exons E, C and A o	AAA59242	21	1037	•	55	
Human adenovirus t	AAT41508	17	480	15.2	56.4	_
Ad2/-ORF6/PGK-CFTR	AAQ68003	15	36335	•	58	_
Human adeno-associ	ABS69881	24	10	15.6	58	Ψ
Adenoviral vector	ABK49009	24	34616	٠	58	w
	AAX07371	20		15.6	58	7
Nucleotide sequenc	AAV27572	19	78	•	ω.	٠,
breast o	ABT10145	24	46275	•		01
Human nervous syst	ABA15585	22	8532	•	ù	
nervo	ABA15407	22	8532	•	ω	w
full-1	AAK94103	22	77		.7	
cDNA clc	AAK93136	22	764		7.	_
n cDNA 5'-	AAK91566	22	764	•		_
receptor inh	AAZ50498	21	312		•	w
ancer-as	ABX76334	25	43	38.3	٠	w
cancer	ACC50112	25	43	38.3		7
cancer	ABL63089	24	2439	38.3	•	٠,
Breast cancer rela	ABL62870	24	43	38.3		٠.
adenoc	ABL62104	24	3	8	٠	-
t cancer	ABT07751		43	8		۳
Human breast cance	ABT10887		43	æ		١٠
COMP/TSP-2	AAA47735	21	Ñ	38.3	•	_
n COMP/TSE	77	21	755	38.3	N	_
KDEL receptor inhi	AAZ50494	21	357	47.7	177.6	•

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Chimeric
Chimeric
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                                                                                                                                                                                                                                    KDEL receptor inhibitor; heat shock protein; immune response; oligomerisation domain; neoplasia; sarcoma; lymphoma; leukaemia; melanoma; carcinoma; glioblastoma; astromytoma; oncogene; infectious disease; allergy; autoimmune disease; ss.
           misc_feature
                                                    mat_peptide
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Camelus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The patent discloses the use of KDEL receptor inhibitor to promote conservation of proteins that are normally retained within the cell such as heat shock proteins by inhibiting KDEL receptor-mediated return of protein complexes to endoplasmic reticulum. This makes the secreted heat shock protein more accessible to the immune system and improves immune response to a target antigen. The inhibitor protein comprises several subunits where each subunit comprises an oligomerisation domain and has at its carboxy terminus a region which binds to a KDEL receptor. The target antigen may be associated with diseases including neoplasia such as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and infectious diseases, allergy or autoimmune diseases. The present sequence encodes KDEL receptor inhibitor comprising regions encoding a cleavable signal peptide; the oligomerisation domain of human cartilage oligomeric matrix protein (COMP) pentamerisation domain, a camel IGG oligomeric matrix protein (COMP) pentamerisation domain, a camel IGG clinker domain and the carboxy-terminal sequence KDEL. The subsequence disculphide bonds.
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                                                      CCGCAGCCGCAGCCGCAGCCGAAACCGCAGCCGAAACCGGAACCGGAAGGTACC
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                               The patent discloses the use of KDEL receptor inhibitor to promote secretion of proteins that are normally retained within the cell such as heat shock proteins by inhibiting KDEL receptor-mediated return of protein complexes to endoplasmic reticulum. This makes the secreted heat shock proteins more accessible to the immune system and improves immune response to a target antigen. The inhibitor protein comprises several subunits where each subunit comprises an oligomerisation domain and has at its carboxy terminus a region which binds to a KDEL receptor. The target antigen may be associated with diseases including neoplasia such as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and astromytoma, with defective tumour suppressor genes, oncogenes, infectious diseases, allergy or autoimmune diseases. The present
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                                                                                                                                                                                                                                                                                          oligomerisation domain; neoplasia; sarcoma; lymphoma; leukaemia; melanoma; carcinoma; glioblastoma; astromytoma; oncogene; infectious disease; allergy; autoimmune disease; ss.
                                                                           misc_feature
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                                                                                                      /note= "Derived .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The patent discloses the use of KDEL receptor inhibitor to promote CC secretion of proteins that are normally retained within the cell such as CC heat shock proteins by inhibiting KDEL receptor-mediated return of CC protein complexes to endoplasmic reticulum. This makes the secreted heat Shock proteins more accessible to the immune system and improves immune CC response to a target antigen. The inhibitor protein comprises several CC subunits where each subunit comprises an oligomerisation domain and has CC at its carboxy terminus a region which binds to a KDEL receptor. The CC target antigen may be associated with diseases including neoplasia such CC as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and CC astromytoma, with defective tumour suppressor genes, oncogenes, CI infectious diseases, allergy or autoimmune diseases. The present CC sequence encodes KDEL receptor inhibitor comprising regions encoding a CC cleavable signal peptide; the oligomerisation domain of human CC thrombospondin 3 (TSP3) trimerisation domain; a camel 1gG linker domain CC and the carboxy-terminal sequence KDEL. The subsequence GDCC is an alteration of rat cartilage oligomeric matrix protein which provides concerns of the carboxy-terminal sequence KDEL.
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                                                                                              CCGCAGCCGCAGCCGCAGCCGCAAACCGCAACCGGAAACCGGAACCGGAACGGTACC 315
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                                                                                                                                                                                                                                                                                                                      TCCAGCCTGGGTGGAGACTGTTTGTTCAGACCTGGGCCCGCAGATGCTTCGGGAACTGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         369 BP;
                                                                                                                                                                                                                                                                                                 TCCAGCCTGGGTGGAGACTGTTGTGGGGAGCCAGACCAAGGCATTGGTCACCCCAGCTCACC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95 A; 105 C; 107 G; 62 T; 0 other;
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Pred. No. 2.3e-50;
0; Mismatches 67;
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 369
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RESULT 4 AAZ50496

192

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The patent discloses the use of KDEL receptor inhibitor to promote secretion of proteins by inhibiting KDEL receptor-mediated return of the heat shock proteins by inhibiting KDEL receptor-mediated return of the protein complexes to endoplasmic reticulum. This makes the secreted heat shock proteins more accessible to the immune system and improves immune thought to a target antigen. The inhibitor protein comprises several comprises to a target antigen. The inhibitor protein comprises several cat its carboxy terminus a region which binds to a KDEL receptor. The carrier antigen may be associated with diseases including neoplasia such as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and serromytoma, with defective tumour suppressor genes, oncogenes, cinfectious diseases, allergy or autoimmune diseases. The present sequence encodes KDEL receptor inhibitor comprising regions encoding a cleavable signal peptide; the oligomerisation domain of Xenopus thrombospondin 4 (7594) trimerisation domain including an additional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric
Chimeric
sub-sequence; a camel IgG linker domain and the carboxy-terminal sequence KDEL. The subsequence GDCC is an alteration of rat cartilage oligomeric matrix protein which provides increased stability via disulphide bonds.
                                                                                                                                                                                                                                                              Disclosure; Fig 5; 87pp; English
                                                                                                                                                                                                                                                                                         Inhibitors of the KDEL receptor which comprises an oligomerization domain useful for promoting secretion of proteins which are normally retained within the cell
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oligomerisation domain; neoplasia; sarcoma; lymphoma; leu
melanoma; carcinoma; glioblastoma; astromytoma; oncogene;
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)B; AAY44962.
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Camelus
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/note= "Xenopus'.
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97..234
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RESULT 5
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Chimeric
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        28-JUL-1999;
                                                                                   misc_feature
                                                                                                                                            mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 369 BP;
                           10-FEB-2000.
                                              WO200006729-A1
                                                                                                                 misc_feature
                                                                                                                                                                          sig_peptide
                                                                                                                                                                                                                                                                                                                   SEE
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                                                                                                                                                                                                                                    Mus sp.
Camelus
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                                                                                                                                                                                                                                                                                                                                    (first entry)
        99WO-US17147
                                                                                                                                                                     /product= 1
10..68
                                                                                    /note= "N
235..306
                                                                                                                  /product= 97..234
                                                                                                                                               /note= '69..336
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10..339
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79.1%;
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"Camel IgG linker domain"
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                                                                                               domain"
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98US-0124671

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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The patent discloses the use of KDEL receptor inhibitor to promote secretion of proteins that are normally retained within the cell such as heat shock proteins by inhibiting KDEL receptor-mediated return of protein complexes to endoplasmic reticulum. This makes the secreted heat shock proteins more accessible to the immune system and improves immune response to a target antigen. The inhibitor protein comprises several subunits where each subunit comprises an oligomerisation domain and has at its carboxy terminus a region which binds to a KDEL receptor. The target antigen may be associated with diseases including neoplasia such as according a lymphoma lenkemia molaroma carriers and shalaroma and second as the second of th
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                               23-MAY-2000
                                                                                   AAZ50492;
                                                                                                                                       AAZ50492 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                         GTACCGGATCATCAGAAAAAGATGAGTTGTAGGCGGCCGCAGAATTCCATATGCATCTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCACCCTCTTCAACCAGATCCTAGTGGAGCTTCGGGACGACCATCCGAGACCAGGTGAAGG
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                                                                                                                                                                                                                                                                                                                                     372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP; 87 A; 103 C; 120 G; 59 T; 0 other;
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                            (first entry)
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77.5%;
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    Mismatches

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Pred. No. 4.7e-37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68;
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Query Match
Best Local Similarity
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                                                                                                                                                                   infectious diseases, allergy or autoimmune diseases. The present sequence encodes KDEL receptor inhibitor comprising regions encoding a cleavable signal peptide; the oligomerisation domain from rat cartilage oligomeric matrix protein, a camel IgG linker domain and the carboxy -terminal sequence KDEL. This is introduced into host cells by suitable
                                                                                                                                                                                                                                                                                      shock proteins more accessible to the immune system and improves immune response to a target antigen. The inhibitor protein comprises several subunits where each subunit comprises an oligomerisation domain and has at its carboxy terminus a region which binds to a KDEL receptor. The target antigen may be associated with diseases including neoplasia such as sercoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and asstromytoma, with defective tumour suppressor genes, oncogenes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inhibitors of the KDEL receptor which comprises an oligomerization domain useful for promoting secretion of proteins which are normally retained within the cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              The patent discloses the use of KDEL receptor inhibitor to promote secretion of proteins that are normally retained within the cell such as heat shock proteins by inhibiting KDEL receptor-mediated return of protein complexes to endoplasmic reticulum. This makes the secreted heat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
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                                                                                              Sequence
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                                                                                              вP;
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98..222
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253..324
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                                                                                                94
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                    52.0%;
81.6%;
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Score 193.4; DB ;
Pred. No. 6.6e-37,
0; Mismatches 20
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                                           DB 21; Length 387;
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lymphoma; leukaemia;
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Matches

249;

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Indels

30;

Gaps

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RESULT 7
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Chimeric -
Chimeric -
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                                                                                                                                                                                                     mat_peptide
                                                                                                                                                                                                                                                               CDS
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                                             29-JUL-1998;
                                                                28-JUL-1999;
                                                                                   10-FEB-2000
                                                                                                      WO200006729-A1
                                                                                                                                                                                                                                  sig_peptide
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                          (SLOK ) SLOAN KETTERING INST CANCER RES
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        JE,
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                                                                                                                                                                                                                                                                                          Rattus sp.
                                                                                                                                                                                                                                                                                                              Mus sp.
                                                                                                                                                                                                                                                                                                     Camelus sp.
        Mayhew M,
                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                  /product= "Mature k
98..222
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                                             98US-0124671
                                                                99WO-US17147.
                                                                                                                                            /*tag= d
/note= "Rat COMP domain'
253..324
                                                                                                                                                                                                     /note= "Derived 69..354
                                                                                                                                                                                                                                 /*tag= a
/product= "KDEL receptor inhibitor protein"
10..68
                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                        note= "Camel IgG linker domain"
                                                                                                                                                                                                                        *tag=
                                                                                                                                                                                                               from mouse
                                                                                                                                                                                  KUEL
                                                                                                                                                                                  receptor inhibitor protein"
                                                                                                                                                                                                              Bip"
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RESULT 8
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XX
AC AAZ5

AAZ50501 standard; DNA;

444 BP

AAZ50501; 23-MAY-2000

(first entry)

KDEL receptor inhibitor-10 DNA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The patent discloses the use of KDEL receptor inhibitor to promote secretion of proteins that are normally retained within the cell such as heat shock proteins by inhibiting KDEL receptor-mediated return of protein complexes to endoplasmic reticulum. This makes the secreted heat shock proteins more accessible to the immune system and improves immune response to a target antigen. The inhibitor protein comprises several subunits where each subunit comprise an oligomerisation domain and has at its carboxy terminus a region which binds to a KDEL receptor. The target antigen may be associated with diseases including neoplasia such as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 387 BP; 93 A; 107 C; 126 G; 61 T; 0 other;
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                           GATGAGTTGTAGGCGGCGCAGAATTCCATATGCATCTCGAG 372
                                                                                                                                                                      CAGCCCGCACGCACCCCCGGTACTAGTCCGCAGCCGCAGCCGAAACCGCAGCCGCAGCCG
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                                                                                                                                                                                                                                                                                                                                                                                        CTTCGGGAACTGCAGGAAACCAACGCGGCGCCTGCAGGACGTGCGGGACTGGCTGCGGCAG 180
GATGAGTTGTAGGCGGCCGCAGAATTCCATATGCATCTCGAG
                                                                                                              CAGCCGCAGCCGAAACCGCAAGCCGAAACCGGAAGCTACCGGATCATCAGAAAAA 330
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                                                                                                                                                                                                                                                                                                                                                  CTTCGAGAACTCCAGGAGACTAATGCGGCGCTGCAAGACGTGAGAGAGCTCTTGCGACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                     GCGGGC--CGAGGGATCCAGCCTGGGTGGAGACTGTTGT------CCACAGATG 105
                                                                                   CAGCCGCAGCCGAAACCGCAGCCGAAACCGGAACCGGAAGGTACCGGATCATCAGAAAAA
                                                                                                                                                                                                                                                            CAGGTCAAGGAGATCACCTTCCTGAAGAATACGGTGATGGAATGTGACGCTTGCGGAATG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGCTTACCATGGGAAAGTTCACTGTGGT-GGCGGCGGCGTTGCTGCTGCTGGGCGCGGT 59
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Pred. No. 1.4e-36;
0; Mismatches 50;
                                                                                                                                                                                                                 GGCCGCAGCCGCAGCCGAAACCGCAGCCGCAGCCG 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 387;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60
                                                                                   345
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Matches
                                                       Query Match
                                                                                                                                                       as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and astromytoma, with defective tunour suppressor genes, oncogenes, infectious diseases, allergy or autoimmune diseases. The present sequence encodes KDEL receptor inhibitor comprising regions encoding a cleavable signal peptide; a myc-tag; an N-glycosylation sequence; the oligomerisation domain of rat cartilage oligomeric matrix protein (COMP); a camel IGG linker domain and the carboxy-terminal sequence KDEL. The subsequence GDCC is an alteration of rat COMP which provides increased stability via disulphide bonds.
                                                                                                                                                                                                                                                                                                                                                                                               shock proteins more accessible to the immune system and improves immune response to a target antigen. The inhibitor protein comprises several subunits where each subunit comprises an oligomerisation domain and has at its carboxy terminus a region which binds to a KDEL receptor. The target antigen may be associated with diseases including neoplasia such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The patent discloses the use of KDEL receptor inhibitor to promote secretion of proteins that are normally retained within the cell such as heat shock proteins by inhibiting KDEL receptor-mediated return of protein complexes to endoplasmic reticulum. This makes the secreted heat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inhibitors of the KDEL receptor which comprises an oligomerization domain useful for promoting secretion of proteins which are normal retained within the cell -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
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                                                                                                           Sequence 444 BP; 115 A; 122 C; 134 G; 73 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 10; 87pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SLOK ) SLOAN KETTERING INST CANCER RES
                                 Local Similarity
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DB; AAY44967.

    Mus sp.
    Rattus sp.
    Camelus sp

        Conservative
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/note= "Rat COMP
310..381
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70..411
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.0..69
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     0,
Score 190.8; DB 21; Length Pred. No. 2.8e-36; 0; Mismatches 22; Indels
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P-PSDB; AAY44960.
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                                                                     Rothman JE,
                                                                                                                                                        29-JUL-1998;
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Best Local
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TSP-1; TSP-2; COMP; cartilage oligomeric matrix protein; thrombospondin; angiogenesis; tumour; treatment; cancer;
                                                      Human COMP/TSP-1 chimeric protein coding sequence.
                                                                                                                                                                       AAA47734 standard; DNA; 755
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                                                                                              08-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          273;
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                                                                                                                                                                                                                                                                                                                                                           GAACCGGAAGGTACCGGATCATCAGAAAAAGATGAGTTGTAGGCGGCCGCAGAATTCCAT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTTCGGGAACTGCAGGAAACCAACGCGGCGCTGCAGGACGTGCGGGACTGGCTGCGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCGGGC--CGAGGGATCCAGCCTGGGTGGAGACTGTTGTAAGGCATTGGTCACCCAG--- 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTGCCAAAAAAGGATCCAGCCTGGGTGGAGACTGTTGTTCAGACCTGGGCCCGCAGATG
                                                                                                                                                                                                                                                                ATGCATCTCGAG
                                                                                                                                                                                                                                                                                                 ATGCATCTCGAG 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGCCGCAGCCGAAACCGCAGCCGCAGCCGCAGCCGAAACCGCAGCCGAAACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGGTCAGGGAGATCACGTTCCTGAAAAAACACGGTGATGGAGTGTGACGCGTGCGGGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGCTTACCATGGGAAAGTTCACTGTGGT-GGCGGCGCGTTGCTGCTGCTGGGCGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGCTTACCATGGGAAGGTACATGATTTTAGGCTTGCTCGCCCTTGCGGCAGTCTGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGGTGAAGGAAATGTCACTCATCCGGAACACCATCATGGAGTGTCAGGTGTGCGGTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.7%;
nilarity 73.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 84 A; 100 C; 114 G; 59 T;
                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCACCCTCTTCAACCAGATCCTAGTGGAGCTTCGGGACGACATCCGAGAC
                                                                                                                                                                                                                                                                357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 177.6; pred. No. 3.8e
                                                                                                                                                                       ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.8e-33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15;
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RESULT 11 AAA47735 ID AAA47 XX

AAA47735 standard; DNA;

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                                                                                                                                                                                                                                                                New nucleic acids are described which encode a protein comprising the second and third type 1 repeats of human TSP (thrombospondin)-1, but not the TGF (transforming growth factor)-beta activation region of human TSP-1. The nucleic acid of TSP (thrombospondin)-1 containing the second and third type-1 repeats and the COMP (cartilage oligomeric matrix protein) assembly sequence (COMP/TSP-1) was produced by PCR (polymerase chain reaction). Expression of COMP/TSP-1 caused inhibition of the growth of tumours in mice models. Thus the nucleic acids and proteins may be useful for treating angiogenesis related diseases such as cancer (by reducing the rate of growth and size of tumours), arthritis, psoriasis, diabetic retinopathy, corneal graft rejection, and glaucoma. They may also be used for treating human immunodeficiency virus (HIV) infection. Anti-angiogenic therapy has little toxicity, does not require the therapeutic agent to enter tumour cells or cross the blood-brain barrier, controls tumour growth independently of growth of tumour cell heterogeneity, and does not induce drug resistance.
                                                                                                                                                                                                 Matches
                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arthritis, psoriasis, diabetic retinopathy, corneal graft rejection, glaucoma, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Fig 4a-b; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding chimeric proteins such as cartilage oligomeric matrix protein (COMP)/thrombospondins (TSP)-1 and 2, useful for
                                                                                                                                                                                                                                                                Sequence 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inhibiting angiogenesis and treating diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lawler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-2000; 2000WO-US02482
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                                                                                                                                                                                                             Local
                              218
                                                                165
                                                                                               158
                                                                                                                                105
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 225
                                                                                                                                                                98
                                                                                                                                                                                                                Similarity
                                                                                                                                                 GTTCAGACCTGGGCCCGCAGATGCTTCGGGAACTGCAGGAAACCAACGCGGCGCTGCAGG 157
                                                                                               ACGTGCGGGACTGCCGGCAGCAGGTCAGGGAGATCACGTTCCTGAAAAAACACGGTGA 217
TGGAGTGTGACGCGTGCGGGATGCAGCAG
                       TGGAGTGTGACGCGTGCGGGCCGCAGCCG
                                                                ACGTGCGGGACTGGCGGCAGCAGGTCAGGGAGATCACGTTCCTGAAAAACACGGTGA
                                                                                                                                GCTCAGACCTGGGCCCGCAGATGCTTCGGGAACTGCAGGAAACCAACGCGGCGCTGCAGG 164
                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                              BP; 147 A; 245 C; 236 G; 127 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISRAEL DEACONESS MEDICAL CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0118053
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26..754
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                                                                                                                                                                                                             38.3%;
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                                                                                                                                                                                               0,
                                                                                                                                                                                             Score 142.6; DB 2
Pred. No. 9.8e-25;
0; Mismatches 4
253
                              246
                                                                                                                                                                                                                            DB_21; Length 755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                such as cancer
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AAA47735;

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Matches
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                                                                                                                                                                                                                                                      angiogenesis related diseases such as cancer (by reducing the rate of growth and size of tumours), arthritis, psoriasis, diabetic retinopathy, corneal graft rejection, and glaucoma. They may also be used for treating human immunodeficiency virus (HIV) infection.

Anti-angiogenic therapy has little toxicity, does not require the therapeutic agent to enter tumour cells or cross the blood-brain barrier, controls tumour growth independently of growth of tumour cell heterogeneity, and does not induce drug resistance.
                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acids are described which encode a protein comprising the second and third type 1 repeats of human TSP (thrombospondin)-1, but not the TGF (transforming growth factor)-beta activation region of human TSP-1. The nucleic acid of TSP (thrombospondin)-1 containing the second and third type-1 repeats and the COMP (cartilage oligomeric matrix protein) assembly sequence (COMP/TSP-1) was produced by PCR (polymerase chain reaction). Expression of COMP/TSP-1 caused inhibition of the growth of tumours in mice models. Thus the nucleic acids and proteins may be useful for treating the produced by the content of the growth of tumours in mice models.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding chimeric proteins such as cartilage oligomeric matrix protein (COMP)/thrombospondins (TSP)-1 and 2, useful for inhibiting angiogenesis and treating diseases such as cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                          Sequence 925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 44; Fig 5a-b; 40pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lawler JW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glaucoma; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thrombospondin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSP-1;
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                                                                                                                                                                              Local
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DB; AAB00041.
                                                                                                                                                            145;
                                                              158
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                                                                                                                             86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TSP-2; COMP; cartilage oligomeric matrix protein; ospondin; angiogenesis; tumour; treatment; cancer; tis; psoriasis; diabetic retinopathy; corneal graft rejection;
                                                                                                                                                                           Similarity
TGGAGTGTGACGCGTGCGGGCCGCAGCCG 246
                                                            ACGTGCGGGACTGCCGGCAGCAGGTCAGGGAGATCACGTTCCTGAAAAAACACGGTGA
                                                                                                              GTTCAGACCTGGGCCCGCAGATGCTTCGGGGAACTGCAGGAAACCAACGCGGCGCTGCAGG
                                                                                              GCTCAGACCTGGGCCCGCAGATGCTTCGGGAACTGCAGGAAACCAACGCGGCGCTGCAGG
                                                                                                                                                                                                                          BP; 156 A; 310 C; 312 G; 147 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0118053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/product= COMP/TSP-2 chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                         38.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                  Pred. No. 1e-2
0; Mismatches
                                                                                                                                                            0,
                                                                                                                                                                       Score 142.6; DB Pred. No. 1e-24;
                                                                                                                                                                                          21;
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                                                                                                                                                            Indels
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RESULT 12
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                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                      The present invention relates to methods of diagnosing breast cancer in a patient, which comprise detecting the level of expression in a tissue sample of two or more genes selected from those shown in ABT09867-ABT11112, where a differential expression of the genes indicates breast cancer. The methods are useful in diagnosing, treating, detecting the progression, and in monitoring treatment of breast cancer in patients. The methods are also useful as a screening tool for agents that modulate the onset or progression of breast cancer. The breast cancer genes may be used as diagnostic markers for the prediction or identification of the malignant state of breast tissue, for confirming the type and progression of cancer, and for drug screening and assays. The present sequence is a coding sequence of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Diagnosing breast cancer in a patient comprises detecting the level of gene expression in cell or tissue samples, where a differential gene expression is indicative of breast cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-JAN-2001; 2001US-263757P.
25-APR-2001; 2001US-286090P.
23-MAY-2001; 2001US-292517P.
                                                                                                                                                                                                                             Sequence 2439 BP; 503 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-674803/72.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; breast specific gene; breast cancer; differential expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human breast cancer associated coding sequence SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABT10887 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENE-)
                                                                                                                                                                                                                                                           ftp.wipo.int/pub.published_pct_sequences.
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                 218
                                               165
                                                                          158
                                                                                                        105
                                                                                                                                      86
                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENE LOGIC INC.
TGGAGTGTGACGCGTGCGGGCCGCAGCCG
                                                                       ACGTGCGGGACTGGCGGCAGCAGGTCAGGGAGATCACGTTCCTGAAAAAACACGGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGAGTGTGACGCGTGCGGGATGCAGCAG
                                             ACGTGCGGGACTGGCTGCGGCAGCAGGTCAGGGAGATCACGTTCCTGAAAAAACACGGTGA
                                                                                                          GCTCAGACCTGGGCCCGCAGATGCTTCGGGAAACTGCAGGAAACCAACGCGGCGCTGCAGG
                                                                                                                                    GTTCAGACCTGGGCCCGCAGATGCTTCGGGAACTGCAGGAAACCAACGCGGCGCTGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nation M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first
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                                                                                                                                                                                 38.3%;
                                                                                                                                                                                                                                758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JC,
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                                                                                                                                                                                 Score 142.6;
Pred. No. 1.:
                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                               809 G;
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                                                                                                                                                                                                                             369 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253
                                                                                                                                                                                  2e-24;
                                                                                                                                                                                                  DB
                                                                                                                                                                                               24;
                                                                                                                                                                    Indels
                                                                                                                                                                                               Length 2439;
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                                                                                                                                                                  Gaps
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RESULT 13
ABT07751
ID ABT077
XX ABT077
XX ABT077
XX ABT077
XX ABT077
XX Gene;
XX Gene;
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                                                                                                                                                                                                                                                                                                                                        The invention comprises a method of detecting a breast cancer-associated CC transcript in a cell from a patient. The method of the invention involves contacting a biological sample from the patient with a nucleotide that the principle of the invention involves CC contacting a biological sample from the patient with a nucleotide that the principle of the form the patient with a nucleotide that cCC in the specification. The method of the invention is useful in the CC diagnosis or prognosis of breast cancer, and for detecting genes that are up or down-regulated in breast cancer cells. Genes identified by the CC targets for screening for therapeutic compounds that modulate breast cancer (e.g. hormones or antibodies). Identification of genes that are cover or under expressed in breast cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics drug development, pharmacogenetics, protein structure and biosensor development. DNA sequences ABT07693 - ABT07761 represent the 69 breast cancer-associated gene sequences of the
                                                                                                                                                                   Matches
                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-APR-2001;
09-APR-2001;
04-MAY-2001;
29-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene;
drug (
                                                                                                                                                                                                                                                                        Sequence 2439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 9; Page 400-401; 410pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detecting a breast cancer-associated transcript in a patient's cell, useful for diagnosing breast cancer, comprises contacting a biological sample with a polynucleotide that selectively hybridizes with breast cancer nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Breast cancer-associated gene sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABT07751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABT07751 standard; DNA; 2439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JAN-2001;
02-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-JAN-2002; 2002WO-US02242.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200259377-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (EOSB-)
                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   development;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2002-583738/62.
     158
                                                        105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ds; breast cancer; breast cancer-associated gene se
development; pharmacogenetics; biosensor development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      225
                                                                                                                                                                   145;
                                                                                                          98
                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABJ05594
                                                  GCTCAGACCTGGGCCCGCAGATGCTTCGGGAACTGCAGGAAACCAACGCGGCGCTGCAGG
                                                                                       GTTCAGACCTGGGCCCGCAGATGCTTCGGGAACTGCAGGAAACCAACGCGGCGCTGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGAGTGTGACGCGTGCGGGATGCAGCAG 253
ACGTGCGGGACTGGCTGCGGCAGCAGGTCAGGGAGATCACGTTCCTGAAAAAACACGGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gigh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; 2001US-263965P.
2001US-265928P.
2001US-282698P.
2001US-0829472.
2001US-288590P.
2001US-294443P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BIOTECHNOLOGY INC
                                                                                                                                                             38.3%;
llarity 97.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                        ВP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KC,
                                                                                                                                                                                                                                                                        503 A; 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Afar D;
                                                                                                                                                             0
                                                                                                                                                             Score 142.6;
Pred. No. 1.2e
0; Mismatches
                                                                                                                                                                                                                                                                        Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВP
                                                                                                                                                                                                                                                                        809 G; 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59
                                                                                                                                                                                         1.2e-24;
                                                                                                                                                                                                                                                                        T; 0
                                                                                                                                                                                                             DB 24; Length
                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                        other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene sequence;
                                                                                                                                                                                                                2439;
                                                                                                                                                             <u>.</u>
                                                                                                                                                          Gaps
217
                                                                                                        157
                                                     164
                                                                                                                                                             0
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RESULT 14
ABL62104
ABL622104
ABL622104
AX ABL622
AX BECOMMAN
AW SCOMMAN
AW SCOMMAN
AW GYCOR
AW GYCO
28-SEP-2000

28-SEP-2000

28-SEP-2000

28-SEP-2000

28-SEP-2000

29-SEP-2000

02-OCT-2000

02-OCT-2000

02-OCT-2000

02-OCT-2000

02-OCT-2000

03-OCT-2000

03-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-SEP-2000;
27-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-SEP-2000;
25-SEP-2000;
25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
26-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUN-2000;
05-JUN-2000;
18-SEP-2000;
18-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        stomach; lur
cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-SEP-2000;
28-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2001; 2001WO-US10838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200194629-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-SEP-2000;
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22-SEP-2000;
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20-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABL62104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABL62104 standard; DNA; 2439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adenocarcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
h; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
atic; gene therapy; antineoplastic; Wilm's tumour; adenocarcin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGAGTGTGACGCGTGCGGGATGCAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGAGTGTGACGCGTGCGGGCCGCAGCCG
                                                                                                                                           2000US-235134P

2000US-23563PP

2000US-23563PP

2000US-235710P

2000US-235720P

2000US-235840P

2000US-235840P

2000US-23603P

2000US-23603P

2000US-23603P

2000US-23603P

2000US-23603P

2000US-236109P

2000US-236109P

2000US-23611P

2000US-236811P

2000US-23681P

2000US-237172PP

2000US-237173PP

2000US-237173PP

2000US-237179PP

2000US-237179PP

2000US-237316PP

2000US-237316PP

2000US-237316PP

2000US-237316PP

2000US-237316PP

2000US-237316PP

2000US-237316PP
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2000US-234552P.
2000US-234509P.
2000US-234567P.
2000US-234923P.
2000US-234923P.
2000US-235077P.
2000US-235077P.
2000US-237598P.
2000US-237604P.
2000US-237606P.
2000US-237608P.
2000US-244867P.
2000US-245084P.
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2000US-233617P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tumour; adenocarcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NO:441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224
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RESULT 15
ABL62870
ID ABL62
XX ABL62
AC ABL62
XX 15-MA
DT 15-MA
XX Humar
KW Stoma
KW Stoma
KW Gytos
KW Gene
XX Homo
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cc anti-neoplastic agent. The method involves exposing cells to a chemical cagent to be tested for anti-neoplastic activity, determining a change in cexpression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL6164 cc ABL70110), or is at least 95% identical to (S), where a change in cexpression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening cc an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a cresult of MI, and the data is sufficient to convey the chemical cc treatment of cancer such as colon, breast, stomach, lung, thyroid, cossphageal, ovarian, kidney, prosetate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, cifiltrating lobular cancer, squamous cell carcinoma, neuroendocrine cc carcinoma, papillary carcinoma and Wilm's tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Young PE,
Soppet DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene
                                                                                                                                                                                                                                                            cytostatic;
                                                                                                                                                                                                                                                                                             stomach;
                                                                                                                                                                                                                                                                                                                                                                                   Breast
                                                                                                                                                                                                                                                                                                                                                                                                                                            15-MAY-2002
30-MAY-2001; 2001WO-US10838.
                                                                                                                   WO200194629-A2
                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL62870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABL62870 standard; DNA; 2439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2439 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID 441; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AVAL-) AVALON PHARM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention describes a method (M1) for screening ineoplastic agent. The method involves exposing cells to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002-188264/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98
                                                                                                                                                                                                                                                                                                                      cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
                                                                                                                                                                                                                                                                                                                                                                                cancer related gene sequence SEQ ID NO:1207.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACGTGCGGGACTGGCTGCGGCAGCAGGTCAGGGAGATCACGTTCCTGAAAAAACACGGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTCAGACCTGGGCCCGCAGATGCTTCGGGAACTGCAGGAAACCAACGCGGCGCTGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGAGTGTGACGCGTGCGGGCCGCAGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTTCAGACCTGGGCCCGCAGATGCTTCGGGAAACTGCAGGAAACCAACGCGGCGCTGCAGG
                                                                                                                                                                                                                                                            lung; prostate; pancreas;
c; gene therapy; antineop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGAGTGTGACGCGTGCGGGATGCAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Augustus M,
Weaver Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                            therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; 758 C; 809 G; 369 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carter KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ,
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Pred. No. 1.2e-24;
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The present invention describes a method (M1) for screening for an CC anti-neoplastic agent. The method involves exposing cells to a chemical CC agent to be tested for anti-neoplastic activity, determining a change in CC expression of at least one gene (I) of a signature gene set, where (I) CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664 CC to ABL70110), or is at least 95% identical to (S), where a change in CC expression is indicative of anti-neoplastic activity. (I) has cytostatic CC activity and can be used in gene therapy. M1 can be used for screening CC an anti-neoplastic agent, and can be used for producing a product which CC is the data collected with respect to the anti-neoplastic agent as a CC result of M1, and the data is sufficient to convey the chemical CC structure and/or properties of the agent. M1 can be used in the CC treatment of cancer such as colon, breast, stomach, lung, thyroid, CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating ductal cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                          29-SEP-2000;
22-SEP-2000;
02-OCT-2000;
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27-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                         Screening for anti-neoplastic agent involves exposing cells to chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature ger
                                                                                                                                                                                                                               Claim 1;
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CC carcinoma, papillary carcinoma and Wilm's tumour.

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Sq Sequence 2439 BP; 503 A; 758 C; 809 G; 369 T; 0 other;

Query Match
Best Local Similarity 97.3%; pred. No. 1.2e-24;
Matches 145; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 98 GTTCAGACCTGGGCCGCAGATGCTTCCGGAACTGCAGGAAACCAACGCGGCTGCAGG 157

Db 105 GCTCAGACCTGGGCCCGCAGATGCTTCCGGAACTGCAGGAAACCAACGCGGCTGCAGG 164

Qy 158 ACGTGCCGGGACTGGCTGCGGCAGCAGGTCAGGAAACCAACGCGGCTGCAGG 217

Db 165 ACGTGCCGGACTGGCTGCGGCAGCAGGTCAGGAAACCACGGTGA 217

Db 165 ACGTGCCGGACTGGCTGCGGCAGCAGGTCAGGAGATCACGTTCCTGAAAAACACGGGTGA 217

Db 165 ACGTGCCGGACTGGCTGCGGCAGCAGGTCAGGAGATCACGTTCCTGAAAAACACGGTGA 224

Qy 218 TGGAGTGTGACGCTGCCGCAGCAGGTCAGGAGATCACGTTCCTGAAAAACACGGTGA 224

Db 225 TGGAGTGTGACGCGTGCGGGAGCAGCAGCAGGTCACGTTCCTGAAAAACACGGTGA 224

Search completed: August 26, 2003, 16:08:06

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is derived by analysis of the total score distribution.
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1. /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2. /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3. /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4. /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5. /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6. /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Gapop 10.0 , Gapext 1.0
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 US-09-124-671-24
US-09-124-671-20
US-09-124-671-20
US-09-124-671-120
US-09-124-671-130
US-09-124-671-16
US-09-124-671-18
US-09-124-671-18
US-09-124-671-18
US-09-124-671-18
US-09-124-671-18
US-09-124-671-26
PCT-US96-04648-1
US-09-128-53-691-3
US-09-181-585-3
US-09-181-585-3
US-09-181-585-3
US-09-181-585-2
US-09-181-585-3
US-09-181-585-3
US-09-181-324-324-324
US-09-664-4218-324
US-09-684-843A-1
US-09-684-843A-1
US-09-684-843A-1
US-09-684-803B-3
US-08-469-803B-3
US-08-461-803B-3
US-08-461-566-111
US-08-461-566-111
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17, Appl

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19, Appl

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301 GAACCGGAAGGTACCGGATCATCAGAAAAAGATGAGTTGTAGGCGGC 	CTTCGGGAACTGCAGGAAACCAACGCGGCGGCGCTGC CAGGTCAGGGAGATCACGTTCCTGAAAAACAACACGG	Ty Match t Local Similarity 100.0%; Score 372; Dt Local Similarity 100.0%; Pred. No. 3e-ches 372; Conservative 0; Mismatches 1 AAGCTTACCATGGGAAGGTACATGATTTTAGGCT	T 1 -124-671-24 -124-671-24 ent No. 6160088 ERAL INFORMATION: PLICANT: Hope, Mee PLICANT: Mayhew, Mark PLICANT: Mayhew, Mark PLICANT: Hoe, Mee PLICANT APPLICATION NUMBER: US/09/124,671A RRENT FILING DATE: 1998-07-29 MMER OF SEQ ID NOS: 42 FTWARE: FastSEQ for Windows Version 3.0 ID NO 24 ENCYTH: 372 PEE DNA RCANISM: Artificial Sequence EATURE: EATURE: HOPORMATION: Chimeric human COMP-KDEL -124-671-24	28 49.8 13.4 336 2 US-07-814-220-4 29 49.8 13.4 336 2 US-07-812-421-4 30 49.6 13.3 10348 2 US-08-457-273B-41 31 49.6 13.3 10348 3 US-08-556-419-13 32 49.6 13.3 10346 1 US-08-246-982A-5 34 49.6 13.3 10366 1 US-08-246-982A-5 35 49.2 13.2 20.3 3 US-08-464-318-12 37 48.4 13.0 71 2 US-08-464-318-12 38 48.4 13.0 71 2 US-08-461-566-12 39 48.2 13.0 33.6 2 US-07-814-220-3 40 48.2 13.0 33.6 2 US-07-814-220-3 41 47.8 12.8 90 1 US-08-461-318-8 42 47.8 12.8 90 2 US-08-461-341-8 43 47.8 12.8 90 2 US-08-461-566-8 44 47.4 12.7 2294 4 US-09-086-663A-7 45 47.4 12.7 3334 4 US-09-086-663A-7
CGGCCGCAGAATTCCAT 36(CGGCCGCAGAATTCCAT 36(PAG 18 CG 24 CG 30 CG 30 CG 30	ength 372; Indels 0; Gaps (CCTTGCGGCAGTCTGCAGC 60		Sequence 4, Appli Sequence 4, Appli Sequence 11, Appl Sequence 13, Appl Sequence 5, Appli Sequence 5, Appli Sequence 7, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 13, Appli Sequence 14, Appli Sequence 18, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 70, Appli Sequence 70, Appli Sequence 71, Appli

240

180 180

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120

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Sequence 28, Application US/09124671A
Patent No. 6166008
GENERAL INFORMATION:
APPLICANT: Rochman, James
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REPERENCE: 31488
CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
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APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
CURRENT APPLICATION UNWBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 30
LENGTH: 372
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Pred. No. 6.1e-57;
0; Mismatches 63;
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GENERAL INFORMATION:
APPLICANT: ROCHMAN, James
APPLICANT: ROCHMAN, Mark
APPLICANT: Hoe, Mee
TIFILE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILLE REFERENCE: 31488
CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 22
LENGTH: 369
TYPE: DNA
ORGANISM: Artificial Sequence
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; OTHER INFORMATION: chimeric Xenopus laevis TSP4-KDEL
US-09-124-671-22
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US-09-124-671-22
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; OTHER INFORMATION: chimeric human TSP3-KDEL
US-09-124-671-28
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                                                                                                Query Match
Best Local Similarity
Matches 239; Conserv
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ORGANISM: Artificial Sequence
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                                 AGGGATCCAGCCTGGGTGGAGACTGTTGTGGTGACGTCAGCAGACAGTTGATTGGCCAGA 127
                                                           AAGGATCCAGCCTGGGTGGAGACTGTTGTTCAGACCTGGGCCCGCAGATGCTTCGGGAAC
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                                                                                                     Conservative
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Pred. No. 3e-40;
0; Mismatches
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Pred. No. 2.1e-55;
Migmatches 67;
                                                                                                                                   DB 3; Length 369
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GENERAL INFORMATION:
APPLICANT: Rothman, James
APPLICANT: Rothman, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 20
LENGTH: 369
TYPE: DNA
ORGANISM: Artificial Sequence
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US-09-124-671-20
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Pred. No. 2.6e-38;
0; Mismatches 68
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                                         ; FEATURE:
; OTHER INFORMATION: chimeric rat
US-09-124-671-16
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Best Local Similarity 81.6%;
Matches 249; Conservative
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Query Match
Best Local Similarity
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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 51.6%;
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 Score 192; DB 3;
Pred. No. 7.8e-38;
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GENERAL INFORMATION:
APPLICANT: Rothman, James
APPLICANT: Rothman, James
APPLICANT: Hoe, Mer
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILLE REFERENCE: 31408
CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 16
LENGTH: 387
TYPE: DNA
ORGANIEM: Artificial Sequence
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APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 14
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Pred. No. 3.6e-38;
COMP-KDEL
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APPLICANT: Rothman, James
APPLICANT: Mayhew, Mark
APPLICANT: Hee, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FAStSEQ for Windows Version 3.0
SEQ ID NO 35
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; Sequence 35, Application US/09124671A
; Patent No. 6160088
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                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                           Query Match 51.3%;
Best Local Similarity 80.6%;
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                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 444
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                         175
                    295
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                                                                                                                                                                                                    GGATCCAGCCTGGGTGGAGACTGTTGT------
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                                                                                             CAGGAGACTAATGCGGCGCTGCAAGACGTGAGAGAGCTCTTGCGACAGCAGGTCAAGGAG
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                                                                            ATCACCTTCCTGAAGAATACGGTGATGGAATGTGACGCTTGCGGAATGCAGCCCGCACGC
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Pred. No. 1.6e-37;
0; Mismatches 22
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US-09-124-671-26
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; Sequence 18, Application
; Patent No. 6160088
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GENERAL INFORMATION:
APPLICANT: ROCHMAN, James
APPLICANT: Mayhew, Mark
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/124,671A CURRENT FILING DATE: 1998-07-29 NUMBER OF SEQ ID NOS: 42 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 18 LENGTH: 357
                                                                        Sequence 26, Application US/09124671A Patent No. 6160088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 3148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 47.7%;
Local Similarity 73.4%;
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                                                                                                                                                                                                                                 GAACCGGAAGGTACCGGATCATCAGAAAAAGATGAGTTGTAGGCGGCCGCAGAATTCCAT
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Pred. No. 2.3e-34;
0; Mismatches 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 357;
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240

225

180 114

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FILE REFERENCE: 31488
CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 26
SEQ ID NO 26
LENGTH: 315
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 71.0
264; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application PC/TUS9604648 GENERAL INFORMATION:
APPLICANT: Cell Genesys, Inc.
                                                              SUFTWARE: Patentin Release #1.0, V CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/04648 FILING DATE: CLASSIFICATION:
                                                                                                                                                                COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PCDOS/MSDOS
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cell Genesys, Inc.
TITLE OF INVENTION: Transplantation of Genetically Modified Cells Having Low Leve
                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                               STREET:
                NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                304
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                                                                                                                                                                                                                                                                                           California
                                                                                                                                                                                                                                                                                                                               4 Embarcadero Center,
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71.0%;
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Cell 23-1
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Pred. No. 2.9e-29;
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                                                                                                                                                                                                                                                                                                                                 Suite 3400
                                                                                                                                                      Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3; Length
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; ORGANISM: human
US-09-253-691-3
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GENERAL INFORMATION:
APPLICANT: KOOD, Michael
APPLICANT: KOOD, Michael
TITLE OF INVENTION: SPINOCEREBELLAR ATAXIA TYPE 8 AND METHODS OF DETECTION
FILE REFERENCE: 11000900101
CURRENT APPLICATION NUMBER: US/09/181,585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Dong Kyu JIN
TITLE OF INVENTION: Diagnostic Method and Kit for Neuropsychiatric
TITLE OF INVENTION: Using Trinucleotide Repeats Sequence
FILE REFERENCE: 1942/36
                                                                                                       Sequence 3, Application US/09181585 Patent No. 6524791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: WordPerfect 6.1/Windows SEQ ID NO 3 LENGTH: 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09253691 Patent No. 6124100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/253,691
CURRENT FILING DATE: 1999-02-22
EARLIER APPLICATION NUMBER: KR 98-6,278
EARLIER FILING DATE: 1996-02-26
NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415494-8771
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 480 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                    232
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                                                                                                                                                                                                                                                                                                                                                                              172 CTGCGGCAGCAGGTCAGGGAGATCACGTTCCTGAAAAACACGGTGATGGAGTGTGACGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 CCGCAGATGCTTCGGGAAACTGCAGGAAACCAACGCGGCGCTGCAGGACGTGCGGGACTGG 171
                                                                                                                                                                                                                                                                                                                                                                                                                        16 AGGTACATGATTTTAGGCTTGCTCGCCCTTGCGGCAGTCTGCAGCGCTGCCAAAAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.2%;
l Similarity 98.3%;
57; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
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                                                                                                                                                                                                                                                                                  TGCGGGCCGCAGCCGCAGCCGAAACCGCAGCCGCAGCCGCAGCCGAAACCCGCAG
                                                                                                                                                                                                                                                                                                                                                     AGGTACATGATTTTAGGCTTGCTCGCCCTTGCGGCAGTCTGCCAGCGCTGCCAAAAAAGG
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53.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 55.4; DB 3; Length 397; Pred. No. 7e-05; 0; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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Pred. No. 4.1e-05;
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US-09-181-585-1/c
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-181-585-1
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; OTHER INFORMATION:
US-09-181-585-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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Best Local Similarity 53.5%;
                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ranum, Laura P.W.
APPLICANT: Koob, Michael
TITLE OF INVENTION: SPINOCEREBELLAR ATAXIA TYPE 8 AND METHODS OF DETECTION
FILE REFERENCE: 11000900101
CURRENT APPLICATION NUMBER: US/09/181,585
CURRENT APPLICATION NUMBER: US/09/181,585
UNMBER OF SEQ ID NOS: 18
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 1998-10-28
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1037
TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
                                                             620
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                                                                                                                                                      CAGGACGTGCGGGACTGGCTGCGGCAGCAGGTCAGGGAGATCACGTTCCTGAAAAACACG
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                             CCGCAGCCGAAACCGCAGCCGAAACCGGAACCGGA 308
                                                             Conservative
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53.5%;
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Pred. No. 0.0001;
0; Mismatches 100; Indels
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US-09-181-585-2/c
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Best Local S
Matches 115
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09181585
Patent No. 6524791
GENERAL INFORMATION:
APPLICANT: Kanum, Laura P.W.
APPLICANT: Koob, Michael
TITLE OF INVENTION: SPINOCEREBELLAR ATAXIA TYPE 8 AND METHODS OF DETECTION PILE REFERENCE: 11000900101
CURRENT APPLICATION NUMBER: US/09/181,585
CURRENT FILING DATE: 198-10-28
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 22
LENGTH. 1411
                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1471
TYPE: DNA
                                                                                                                                                                                                                                                               y Match
Local Similarity 53.5%;
hes 115; Conservative
1182
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CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA 1148
                               CCGCAGCCGAAACCGCAGCCGAAACCGGAACCGGA 308
                                                               GTGATGGAGTGTGACGCGTGCGGGCCGCAGCCGCAGCCGAAACCGCAGCCGCAGCCGCAG
                                                                                                                                 CAGGACGTGCGGGACTGGCTGCGGCAGCAGGTCAGGGAGATCACGTTCCTGAAAAACACG
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Pred. No. 0.00011;
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Search completed: August 26, 2003, 15:35:31 Job time: 56 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                    No.
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                                                                                                                                                                 142.6
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1: /cgn2 6/ptodata/1/pubpna/US07 PUBCOMB.seq:*

2: /cgn2 6/ptodata/1/pubpna/US06 NEW PUB.seq:*

3: /cgn2 6/ptodata/1/pubpna/US06 NEW PUB.seq:*

4: /cgn2 6/ptodata/1/pubpna/US07 PUBCOMB.seq:*

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6: /cgn2 6/ptodata/1/pubpna/US08 PUBCOMB.seq:*

7: /cgn2 6/ptodata/1/pubpna/US08 PUBCOMB.seq:*

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10: /cgn2 6/ptodata/1/pubpna/US09 PUBCOMB.seq:*

11: /cgn2 6/ptodata/1/pubpna/US09 PUBCOMB.seq:*

12: /cgn2 6/ptodata/1/pubpna/US09 PUBCOMB.seq:*

13: /cgn2 6/ptodata/1/pubpna/US09 PUBCOMB.seq:*

14: /cgn2 6/ptodata/1/pubpna/US09 PUBCOMB.seq:*

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17: /cgn2 6/ptodata/1/pubpna/US08 PUBCOMB.seq:*

16: /cgn2 6/ptodata/1/pubpna/US08 PUBCOMB.seq:*

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16: /cgn2 6/ptodata/1/pubpna/US08 PUBCOMB.seq:*
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Match
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372
1 aagcttaccatgggaaggta.....aattccatatgcatctcgag 372
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                        1517243 seqs, 1124081882 residues
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       9025608
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                                                                                                               2439
2439
2439
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34427
35937
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   10 US-09-919-603-4
10 US-09-919-603-6
10 US-09-954-531-359
10 US-09-954-531-359
11 US-09-918-6248-49
12 US-10-301-822-40
14 US-10-177-293-71
10 US-09-718-718A-3
14 US-10-156-761-4994
11 US-09-918-995-4559
11 US-09-918-995-4560
12 US-09-735-705-324
10 US-09-778-324
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Sequence 4, Appli
Sequence 6, Appli
Sequence 140, App
Sequence 359, App
Sequence 49, Appl
Sequence 40, Appl
Sequence 71, Appli
Sequence 5, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 4559, Ap
Sequence 4560, Appli
Sequence 4560, App
Sequence 324, App
Sequence 324, App
Sequence 324, App
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<u>4</u> 5	44	43	42	41	40	39	38	37	36	ω 5	34	ω u	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
46.2	46.2	46.2	46.2	46.2	46.2	46.2	46.2	46.2	46.2	46.2	46.2	46.4	46.4	46.4	46.4	46.4	47.8	48.2	49.6	49.6	50.6	51.2	51.2	52.6	53	53	53	53
12.4	12.4	12.4	12.4	12.4	12.4	12.4	12.4	12.4	12.4	12.4	12.4	12.5	12.5	12.5	12.5	12.5	12.8	13.0	13.3	13.3	13.6	13.8	13.8	14.1	14.2	14.2	14.2	14.2
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US-10-141-704-9	US-10-141-702-9	US-10-141-698-9	-10	US-10-140-924-9	US-10-140-922-9	US-10-140-807-9	US-10-140-471-9	US-10-140-274-9	US-10-140-021-9	US-10-140-018-9	US-10-137-870-9	US-10-291-249-14	US-10-291-230-14	US-09-880-107-1748	US-09-822-846-491	US-10-294-804-3	US-10-079-623-187	US-10-215-432-26		US-10-215-432-30	US-10-156-761-1	US-09-976-059-1	US-10-080-797-14	US-09-967-768A-116	US-10-071-766-33	US-10-301-822-154	US-09-925-301-441	US-10-117-982-324
9	Sequence 9, Appli	9	,	,	Sequence 9, Appli	9	Sequence 9, Appli	٥	Sequence 9, Appli	œ,	Sequence 9, Appli	14,	14,	1748,	49	Sequence 3, Appli	Sequence 187, App	Sequence 26, Appl	31	ö,	Sequence 1, Appli	1, 1	Sequence 14, Appl	116,	33,	e 154,	Sequence 441, App	e 324,

FILE REFERENCE: 1440.1033-007 CURRENT APPLICATION NUMBER: US/09/919.603 CURRENT FILING DATE: 2001-07-30 PRIOR APPLICATION NUMBER: PCT/US00/02482 PRIOR FILING DATE: 2000-02-01 PRIOR APPLICATION NUMBER: 60/118,053 PRIOR FILING DATE: 1999-02-01 NUMBER OF SEQ ID NOS: 21 SOPTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 4 LENGTH: 755 ; OTHER INFORMATION: fusion gene US-09-919-603-4 US-09-919-603-4 GENERAL INFORMATION: John W. APPLICANT: Lawler, John W. TITLE OF INVENTION: COMP/TSP-1, COMP/TSP-2 and Other TSP TITLE OF INVENTION: Chimeric Proteins Sequence 4, Application US/09919603 Patent No. US20020137679A1 TYPE: DNA ORGANISM: Artificial Sequence FEATURE:

ALIGNMENTS

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105 GCTCAGACCTGGGCCCGCAGATGCTTCGGGAACTGCAGGAAACCAACGCGGCGCTGCAGG

GTTCAGACCTGGGCCCGCAGATGCTTCGGGAACTGCAGGAAACCCAACGCGGCGCTGCAGG

ACGTGCGGGACTGCCGGCCAGCAGGTCAGGGAGATCACGTTCCTGAAAAAACACGGTGA

217 224

164

ACGTGCGGGACTGGCGGCAGCAGGTCAGGGAGATCACGTTCCTGAAAAAACACGGTGA

158

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98

Query Match Best Local Similarity Matches 145; Conserv

Conservative

38.3%;

Score 142.6; DB 10; pred. No. 3.7e-32; 0; Mismatches 4;

Indels Length 755;

0,

Gaps

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218

TGGAGTGTGACGCGTGCGGGCCGCAGCCG 246

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APPLICANT: Weaver, Zoe
APPLICANT: Weaver, Zoe
TITLE OF INVENTION: Gene Sets
FILE REFERENCE: 68920-77
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: US/60/233,133
PRIOR APPLICATION NUMBER: US/60/233,133
PRIOR APPLICATION NUMBER: US/60/234,009
PRIOR APPLICATION NUMBER: US/60/234,009
PRIOR APPLICATION NUMBER: US/60/234,009
PRIOR APPLICATION NUMBER: US/60/234,009
PRIOR APPLICATION NUMBER: US/60/234,034
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,509
PRIOR APPLICATION NUMBER: US/60/234,509
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US/60/234,509
PRIOR APPLICATION NUMBER: US/60/234,509
PRIOR APPLICATION NUMBER: US/60/234,509
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 2000-09-22
PRIOR SEQ ID NOS: 1392
COMPTUDED: DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 1392
; TYPE: DNA
; ORGANISM: Homo sapiens
US *09-954-531-140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
US-09-954-531-140
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TITLE OF INVENTION: COMP/TSP-1, COMP/TSP-2 and Otl
TITLE OF INVENTION: Chimeric Proteins
FILE REFERENCE: 1440.1033-007
CURRENT APPLICATION NUMBER: US/09/919,603
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: PCT/US00/02482
PRIOR FILING DATE: 2000-02-01
PRIOR FILING DATE: 2000-02-01
PRIOR FILING DATE: 1999-02-01
PRIOR FILING DATE: 1999-02-01
VOUNBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: fusion gene US-09-919-603-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. US20020165180A1
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Best Local Similarity
                                                                                                        SOFTWARE: Pa
SEQ ID NO 140
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH: 925
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                                                                                 2439
                                                                                                                                 PatentIn version 3.0
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97.3%;
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Pred. No. 3.8e-32;
0; Mismatches 4
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RESULT 5
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CURRENT APPLICATION NUMBER: US/09/954,531

CURRENT FILING DATE: 2002-05-02

PRIOR APPLICATION NUMBER: US/60/233,133

PRIOR FILING DATE: 2000-09-18

PRIOR APPLICATION NUMBER: US/60/234,009

PRIOR FILING DATE: 2000-09-20

PRIOR APPLICATION NUMBER: US/60/234,034

PRIOR APPLICATION NUMBER: US/60/234,034

PRIOR APPLICATION NUMBER: US/60/234,509

PRIOR FILING DATE: 2000-09-20

PRIOR FILING DATE: 2000-09-20

PRIOR APPLICATION NUMBER: US/60/234,509

PRIOR APPLICATION NUMBER: US/60/234,567

PRIOR APPLICATION NUMBER: US/60/234,567
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Sequence 49, Application US/09918624B publication No. US20030113720A1 GENERAL INFORMATION: APPLICANT: Schebye, Xiao Min APPLICANT: SCOTNASSE, Thierry TITLE OF INVENTION: CDNAS EXPRESSED : FILE REFERENCE: PA-0033 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION: APPLICANT: Weaver,
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Best Local Similarity
Matches 145; Conserv
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Best Local Similarity
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Patent No. US200:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 1392
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20020165180A1
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Pred. No. 4.6e-32;
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                                                                                                                   ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (26)...(2299)
US-10-301-822-40
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PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PERL Program
SEQ ID NO 49
LENGTH: 2439
TYPE: DNA
                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                       SEQ ID NO 40
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                                           Matches
                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/301,822
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kamatkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENE J.
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION,
TITLE OF INVENTION: THERAPY OF COLON CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Millennium Pharmaceuticals, Inc. APPLICANT: Berger, Allison APPLICANT: Guillemette, Tracy L.
                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
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CURRENT FILING DATE: 2002-12-03
                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: MPM01-029P2RNM
                                                                                                                                                                                                    LENGTH: 2439
TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
OTHER INFORMATION: GenBank ID No. US20030113720A1 g602449
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                                         145; Conservative
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GTTCAGACCTGGGCCGCAGATGCTTCGGGAACTGCAGGAAACCAACGCGGCGCTGCAGG 157
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No. US20030148410A1
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                                                            38.3%;
97.3%;
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Pred. No. 4.6e-32;
0; Mismatches 4
                                         0; Mismatches
                                                          Score 142.6; DB 12;
Pred. No. 4.6e-32;
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                                                                              Length 2439;
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; ORGANISM: Homo
US-10-177-293-71
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SEQ ID NO 71
LENGTH: 2439
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Publication No. US20030124128A1
                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/xxx,xxx PRIOR FILING DATE: 2002-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/362,585 PRIOR FILING DATE: 2002-03-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/325,002 PRIOR FILING DATE: 2001-09-25
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CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 60/299,887
PRIOR FILING DATE: 2001-06-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Sahin, Aysegul
APPLICANT: Mills, Gordon B.
TITLE OF INVENTION: COMPOSITIONS,
TITLE OF INVENTION: PREVENTION, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/306,501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: MRI-038
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                                                        158 ACGTGCGGGACTGGCTGCGGCAGCAGGTCAGGGAGATCACGTTCCTGAAAAAACACGGTGA
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218 TGGAGTGTGACGCGTGCGGGCCGCAGCCG 246
                                                                                                               105 GCTCAGACCTGGGCCCGCAGATGCTTCGGGAAACTGCAGGAAACCAACGCGGCGCTGCAGG
                                                                                                                                   98 GTTCAGACCTGGGCCCGCAGATGCTTCGGGAACTGCAGGAAACCAACGCGGCGCTGCAGG
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Hoersch, Sebastian
Monahan, John
Meyers, Rachel E.
Bast Jr., Robert C.
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                                     ACGTGCGGGACTGCCGGCAGCAGGTCAGGGAGATCACGTTCCTGAAAAACACGGTGA
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Mertens, Maureen
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                                                                                                                                                                                    Score 142.6; DB 1
Pred. No. 4.6e-32;
0; Mismatches 4
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                                                                                                                                                                                                                         DB 14;
                                                                                                                                                                                                                         Length 2439;
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TGGAGTGTGACGCGTGCGGGATGCAGCAG 253

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APPLICANT: Hearing, Patrick
APPLICANT: Bahou, Wadie
APPLICANT: Bahou, Wadie
APPLICANT: Sandalon, Ziv
APPLICANT: Gnatenko, Dmitri
TITLE OF INVENTION: Adenoviral Vectors
FILE REFERENCE: STONYB-04970
CURRENT APPLICATION NUMBER: US/09/782,378A
CURRENT FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: 60/237,747
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
SEQ ID NO 3
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                                                                                                                                                                                                                                                                   ; LENGTH: 35937
; TYPE: DNA
; ORGANISM: Human adeno-associated virus
US-09-782-378A-3
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US-09-111-911-5/c
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Publication No. US20030096768A1
GENERRAL INFORMATION:
APPLICANT: Wold, William S.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                  Matches
                                                                                                                                                                                                    Query Match
Best Local Similarity
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SEQ ID NO 5
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CURRENT APPLICATION NUMBER: US/09/111,911
CURRENT FILING DATE: 1998-07-08
NUMBER OF SECID NOS: 5
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                          28807 CCAAGATGAGGTACATGATTTTAGGCTTGCTCGCCCTTGCGGCAGTCTGCAGCGCTGCCA 28866
         28867
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                                                 68 AAAAAG 73
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                                                                                                                                                                                61; Conservative
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                                                                                                                     8 CCATGGGAAGGTACATGATTTTAGGCTTGCCTCGCCCTTGCGGCAGTCTGCAGCGCTGCCA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 CCATGGGAAGGTACATGATTTTAGGCTTGCTCGCCCTTGCGGCAGTCTGCAGCGCTGCCA 67
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         AAAAGG 28872
                                                                                                                                                                                                    15.6%;
                                                                                                                                                                           Score 58; DB 10;
Pred. No. 5.1e-07;
0; Mismatches 5
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; NAME/KEY: CDS
; LOCATION: (1)..(1734)
US-10-156-761-4994
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US-10-156-761-4994
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APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR PILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
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APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
FULE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UF 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROS
APPLICANT: SHIBA, TADAYOSH
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROS
APPLICANT: SHIBA, TADAYOSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                          NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 62; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: JP 2001-272697 PRIOR FILING DATE: 2001-08-02
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                                                                                     ORGANISM: Streptomyces avermitilis
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TYPE: DNA
  OTHER INFORMATION: a, t,
                    NAME/KEY: misc_feature
LOCATION: (4187715)
                                                                     FEATURE:
                                                                                                                                 LENGTH:
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                                                                                                                                      9025608
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HORIKAWA, HIROSHI
SHIBA, TADAYOSHI
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HORIKAWA, HIROSHI
SHIBA, TADAYOSHI
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c, g, other or unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 57.8; DB 14;
Pred. No. 3.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1734;
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; Sequence 4560, Application US/09918995
; Publication NO. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBT
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
                                                                                                                                                                                                              RESULT 13
US-09-918-995-4560
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; NAME/KEY: misc feature

; LOCATION: (1)...(428)

; OTHER INFORMATION: n = A,T,C or

US-09-918-995-4559
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US-09-918-995-4559
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Best Local Similarity 55.7%;
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TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/9/235,076
PRIOR APPLICATION NUMBER: US/9/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 3.0
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCAGCAGGTCAGGGAGATCACGTTCCTGAAAAACACGGTGATGGAGTGTGACGCGTGCG
                                                                                                                                                                                                                                                                                                      AGCAG 252
                                                                                                                                                                                                                                                                                                                                           AACCG 300
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Pred. No. 3.5e-06;
0; Mismatches 82;
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NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for W
SEQ ID NO 324
LENGTH: 521
TYPE: DNA
ORGANISM: Homo sapien
US-09-735-705-324
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US-09-918-995-4560
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                                                                                                                                                                                 Matches
                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT: McNeill, Patricia D.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILLING DATE: 2000-12-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                Local Similarity
                                   112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 AGATGCTTCGGGAACTGCAGGAAACCAACGCGGCGCTGCAGGACGTGCGGGACTGGCTGC
 269 CGCAGCCGCAGCCGAAACCGCAGCCGAAACCGGAACC 305
                                                                     209 ACACGGTGATGGAGTGTGACGCGTGCGGGCCGCAGCCGAACCCGCAGCCGCAGC
                                                                                                                                          149 CGCTGCAGGACGTGCGGGACTGGCTGCGGCAGCAGGTCAGGGAGATCACGTTCCTGAAAA 208
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o. US20020052329A1
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                                                                                                          52
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                                   AGAAGCAGCAGCACCTGGTCCAGCAGCAGCCCCCCCTCGCAGCCGCAGCCGCAGCCGCAGC
                                                                                                          CGCTGCAGATGGTGCAGTACAAGAATCGTCAGGCCATCCTGGCGGTCAAATCCACGCGGC 111
                                                                                                                                                                                                                                                                                                                                          FastSEQ for Windows Version 3.0
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Skeiky, Yasir A.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bangur, Chaitanya
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Fan, Liqun
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Pred. No. 3.5e-06;
0; Mismatches 82
                                                                                                                                                                             Score 53; DB 9;
Pred. No. 6.3e-06;
0; Mismatches 65
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                                                                                                                                                                                                               Length 521
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RESULT 15

US-09-850-716A-324
; Sequence 324, Application US/09850716A
; Patent No. US20020113139A1
; Patent No. US20020113139A1
; PAPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 324
; LENGTH: 521
; TYPE DNA
; ORGANISM: Homo sapien
Search completed: August 26, 2003, 16:55:26 Job time : 822 secs
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                                                                                                                   269 CGCAGCCGCAGCCGAAACCGCAGCCGAAACCGGAACC 305
                                                                                                                                                                    112 AGAAGCAGCAGCACCTGGTCCAGCAGCCCCCCCCCCGCAGCCGCAGCCGCAGCCGCAGC
                                                                                                                                                                                                                                                                                      149 CGCTGCAGGACGTGCGGGACTGGCTGCCGGCAGCAGGTCAGGGAGATCACGTTCCTGAAAA 208
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OM nucleic - nucleic search, using sw model
                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                     Score
 137.8
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length: 2000000000
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Match
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37.0
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99056	BG89905	12	402	.7	.7	w
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)A47-1-	BG89655	12	401	.7	.7	Ψ
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896390 HOA30-1-	G8963	12	J	7		w
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TITLE JOURNAL COMMENT RESULT 1 AI751993 LOCUS DEFINITION REFERENCE AUTHORS SOURCE ORGANISM ACCESSION VERSION KEYWORDS אנאט בא של מאט. בא בא מחוו מאט מאט. בא מרוו מאט Medical Genetics Branch National Human Genome Research Institute 10/10C101, 9000 Rockville Pike, Bethesda, Tel: 301-402-4877 Fax: 301-496-7157 Jia,L.B., Young,M.F., Touchman,J.W., Bouffard,G.G., Beckstrom-Sternberg,S.M., Green,E.D., Powell,J.I., P.G., Hotchkiss,R.N. and Francomano,C.A. SGAP: The Skeletal Genome Anatomy Project Unpublished Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 328) Jia,L.B., Young,M.F., Touchman,J.W., Bouffard,G.G., Homo sapiens AI751993 AI751993.1 GI:5130257 Contact: Libin Jia Homo sapiens (human) Yang, L.M., Robey

ALIGNMENTS

Email: libin@helix.nih.gov DNA Sequencing and analyses by National Institutes of Health Intramural Sequencing Center (NISC).

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20892-1267,

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HOA42-1-H5 HOA
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nilarity 95.3%;
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                                                                                                                      sanjay.
/organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/tissue_type="Cartilage"
/lab_host="E.coli DH10 B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone lib="Normal Human Trabecular Bone Cells" /note="Organ: Hip; Vector: pBluescript; Site 1: Library constructed by Dr. Marian Young and Dr. Gehron Robey (NIDCR)"
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/lab_host="SURE"
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/mol_type="mRNA"

/db_xref="taxon:9606"
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|sex="Female"
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1 (bases 1 to 366)

Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J., Sathe, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and Lark, M.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries Osteoarthr. Cartil. 9 (7), 641-653 (2001)
                                                                                                                                                                                                                                                                                                                                                 Tel: 610-270-7245
Fax: 610-270-5598
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709 Swedeland Road,
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/note="Vector: pSPORT I; Site_1: Sall; Site_2: NotI;
Directional"
123 c 121 g 56 t
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134 c
                                                                                                                                                                  /tissue_type="cartilage"
/lab_host="E.Coli DH10 B"
/clone lib="HOA (Human Osteoarthritic Cartilage)"
/colone lib="HOA (Human Osteoarthritic Cartilage)"
/note="Vector: pSPORT I; Site_1: SalI; Site_2: Not
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|mol_type="mRNA"
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RESULT 5
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709 Swedeland Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries Osteoarthr. Cartil. 9 (7), 641-653 (2001)
 BG897214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Sanjay Kumar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sanjay_kumar-1@gsk.com
imer: T7.
                                                                                                                                                                                                                                                                                                                                Directional"
128 c
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/lab_host="E.coli DH10 B"
/lab_host="E.coli DH10 B"
/clone_lib="HOA (Human Osteoarthritic Cartilage)"
/note="Tector; pSPORT I; Site_1: SalI; Site_2: Not
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'mol_type="mRNA"
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Pred. No. 4.2e-22;
0; Mismatches 7;
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RESULT 6
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MEDLINE
PUBMED
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Best Local (
                                                                             ORGANISM
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1 (bases 1 to 371)
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao, Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. a
                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                 Homo sapiens
                                                                                                                EST
                                                                                                                             BG898406
BG898406.1 GI:14308655
                                                                                                                                                          mRNA sequence.
                                                                                                                                                                          BG898406
HOA8-1-F10 HOA (Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 610-270-5598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         709 Swedeland Road,
Tel: 610-270-7245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlaxoSmithKline
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Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,
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1. (bases 1 to 370)
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BG897214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="cartilage"
/lab host="2.coli DH10 B"
/clone_lib="HOA (Human Osteoarthritic Cartilage)"
/note="Vector: pSPORT I; Site_1: SalI; Site_2: Not
Directional"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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95.3%;
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Osteoarthritic
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e,J.C., Gowen,
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Lark,M.W.

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VERSION
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           UW2109
GlaxoSmithKline
709 Swedeland Road,
Tel: 610-270-7245
Fax: 610-270-5598
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Osteoarthr. Cartil. 9 (7), 641-653 (2001)
                                                                                                                      Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries Osteoarthr. Cartil. 9 (7), 641-653 (2001)
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1 (bases 1 to 372)
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Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay kumar-l@gsk.com
Seq primer: T7.
                                                                               Contact: Sanjay
                                                                                                                                                                                         Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.
                                                                                                                                                                                                                                                             Homo sapiens
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sanjay_kumar-1@gsk.com
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/db_xref="taxon:9666"
/tissue_type="cartilage"
/lab_host="E.coli_DH10_B"
/clome_lib="HOA (Human Osteoarthritic Cartilage)"
/note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
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95.3%;
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Pred. No. 4.2e-22;
0; Mismatches 7;
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mRNA sequence.
BG896387
BG896387.1 GI:
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Tel: 610-270-7245
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                                                                                                                                                                                                                  Email: sanjay_kumar-1@gsk.com
Seq primer: T7
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/db_xref="taxon:9606"
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/lab_host="E.coli DH10 B"
/clone_lib="MOA (Human Osteoarthritic Cartilage)"
/note="Vector: pSPORT I; Site_1: Sall; Site_2: Not
Directional"
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/clone_lib="NoA (Human Osteoarthritic Cartilage)"
/note="Vector: pSPORT I, Site_1: SalI, Site_2: NotI,
Directional"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Sanjay Kumar
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Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen
                                                                                                                                                                                                                                                                                                                                                                                Email: sanjay kumar-1@gsk.com
Seq primer: T7.
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/mol type="mRNA"
/db_xref="ftaxon:9606"
/tissue type="cartilage"
/lab_host="E.coli DH10 B"
/clone lib="HOA (Human Osteoarthritic Cartilage)"
/note="Vector: pSPORT I; Site_1: Sall; Site_2: Not Directional"
129 c 118 g 57 t
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Pred. No. 4.2e-22;
                                                                                                                                         Score 137.8;
Pred. No. 4.2
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Gowen,M. and
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BG900556
HOA42-1-C6 HOA (
mRNA sequence.
                                                                                                                                                                                                                                                                                              98
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DNA Sequencing and analyses by National Institutes
Intramural Sequencing Center (NISC).
Plate: 20 row: g column: 10
Seq primer: M13RP1 reverse primer (ABI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Libin Jia
Medical Genetics Branch
National Human Genome Research Institute
10/10C101, 9000 Rockville Pike, Bethesda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jia,L.B., Young,M.F., Touchman,J.W., Bouffard,G.G., Beckstrom-Sternberg,S.M., Green,B.D., Powell,J.I., P.G., Hotchkiss,R.N. and Francomano,C.A. SGAP: The Skeletal Genome Anatomy Project
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Mammalia; Butheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 374)
Jia,L.B., Young,M.F., Touchman,J.W., Bouffard,G.G.,
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/mol type="mRNA"
/db_xref="taxon:9606"
/clone="NHTBC_cn20g10"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="Normal Human Trabecular Bone Cells" /note="Organ: Hip; Vector: pBluescript; Site 1: Library constructed by Dr. Marian Young and Dr. Gehron Robey (NIDCR)" a 138 c 124 g 57 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Bone"
/cell_type="Trabecular Bone Cells"
/lab_host="SURE"
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(Human Osteoarthritic
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Pred. No. 4.2e-22;
0; Mismatches 7;
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RESULT 12
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HOA20-1-H3 HOA (Human Os
mRNA sequence.
BG898027
BG898027.1 GI:14308276
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Sathe,G.,
                         Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. a
Lark,M.W.
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                                                                                                          Homo sapiens (human)
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Mammalia; Eutheria;
1 (bases 1 to 375)
            Identification
                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  709 Swedeland Road,
Tel: 610-270-7245
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primer: T7.
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, Mui, P., Agarwal, P., Badger, A.M., Lee, J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"

/mol_type="mRNA"
/db_xref="taxon:9668"
/tissue_type="cartilage"
/lab_host="E.coli_DH10_B"
/clone_lib="HOA (Human Osteoarthritic Cartilage)"
/note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
Directional"
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Pred. No. 4.2e-22;
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characterization of 5000 from adult human normal a
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Gowen, M. a
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Query Match
Best Local Similarity 95.3
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                                                                                                                            Contact: Sanjay Kumar
UW2109
                                                                                                                                                                                                Identification and initial characterization sequenced tags (ESTs) each from adult human osteoarthritic cartilage cDNA libraries Osteoarthr. Cartil. 9 (7), 641-653 (2001)
                                                                                                                                                                                                                                                                          Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M.,
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,
Lark,M.W.
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Tel: 610-270-7245
Fax: 610-270-5598
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                Email: sanjay_kumar-1@gsk.com
Seq primer: T7.
                                                      Tel: 610-270-7245
Fax: 610-270-5598
                                                                                                             GlaxoSmithKline
                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 380)
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                                                                                        709 Swedeland Road,
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/lab_host="s.coli DH10 B"
/clone_lib="HOA (Human Osteoarthritic Cartilage)"
/note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
Directional"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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RESULT 14
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1 (bases 1 to 381)
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BG900343.1
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381 bp mRNA linear HOA37-1-F6 HOA (Human Osteoarthritic Cartilage) Ho
                                                                                                                                                                                                                              Email: sanjay kumar-1@gsk.com
Seo primer: T7.
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Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M.
                                                                                                                                                                                                                                                                                                                                          Contact: Sanjay Kumar
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/tissue_type="cartilage"
/lishost="E.coli_DH10_B"
/clone_lib="HOA (Human Osteoarthritic Cartilage)
/note="Vector: pSPORT I; Site_1: SalI; Site_2: N
Directional"
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/lab_host="E.coli DH10 B"
/clone_lib="HOA (Human Osteoarthritic Cartilage)."
/note="Vector: pSPORT I; Site_1: Sall; Site_2: NotI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: sanjay_kumar-1@gsk.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 610-270-7245
Fax: 610-270-5598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    709 Swedeland Road,
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Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Le
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/lab_host="E.coli DH10 B"
/clone lib="HOA. (Human Osteoarthritic Cartilage)"
/cnote="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                    Score 137.8; DB 12;
Pred. No. 4.2e-22;
0; Mismatches 7;
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Db 304 TGGAGTGTGACGGTGCCGGATGCACCAG 332
Search completed: August 26, 2003, 15:34:29
Job time: 1434 secs

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Result No.

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Command line parameters:

-MODEL=frame+ n2p, model -DEV=xlp
-Q=/Cgn2_1/USPTO_spool/US08696872/runat_26082003_150541_8713/app_query.fasta_1.519
-DB=A_Geneseq_19Jun03 -QFMT=fastan -SUFFIX=rag -MINNATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=-LOCAL -OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXILEN=200000000
-USER-US09696872_0CGN 1 1 117 @runat 26082003 150541_8713 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQÜERY -NEG_SCORES=0 -MAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN INDEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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A_Geneseq_19Jun03:*

//SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

//SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

//SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*

//SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

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//SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*

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Copyright (c) 1993 - 2003 Compugen Ltd
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2001.569 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

144.5 142.5 138 133 129.5 126.5 126.5 126.5 123.5 123.5 123.5 123.5 123.5 123.5 146 146 146 146 145.5 145.5 153 146.5 Score Query Match Length DB 1357 889 35 35 54 57 776 961 961 24 622 90 242 300 757 757 757 757 757 ij AAR49650 AAR49752 AAR497536 AAR49536 AAR5624 AAR56324 AAC85036 AAO18488 AAO18488 AAO18488 AAO18488 AAU80744 AAU27733 AAM78731 ABG04441 AAY44950 AAY44947 AAY44946 AAM79715 AAY44963 AAY44959 AAY44965 AAY44965 AAY44967 AAY44967 AAY44968 AAE14307 AAE14305 ABU56605 ABB82286 ABR47420 AAY44964 AAR56248 АВJ05594 AAB00044 AAB00041 SUMMARIES Sequence of hinge Camel 2-chain 1g h Sequence of a pept Camel 1g 2-heavy c Human protein SEO Human thrombospond Human thrombospond Target peptide #6 Human protein SEO Human TSP4 pentame 13P4 pentame 13P4 pentame Human TSP4 pentame Plasmodium berghei Sugarcane proline Sugarcane proline Sugarcane proline Linker peptide #2 Human full-length Human protein SEQ Human thrombospond Human polypeptide, Human cartilage ol Rat cartilage olig Human protein SEQ Xenopus thrombospo KDEL réceptor inhi KDEL receptor inhi HUMAN (COMP/TSP-1 c Human COMP/TSP-2 c Human cartilage ol KDEL receptor KDEL receptor KDEL receptor Description Human protein SEQ Novel human diagno Human thrombospond Breast cancer-asso Breast cancer asso BOP1 protein. PRP 378. Tri KDEL receptor Lung cancer-associ KDEL receptor Triticum inhi inhi inhi

ALIGNMENTS

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Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                       Alignment Scores:
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                            GAAACCAACGCGGCGCTGCAGGACGTGCGGGACTGGCTGCGGCAGCAGGTCAGGGAGATC 195
                                                                          TCCAGCCTGGGTGGAGACTGTTGTTCAGACCTGGGCCCGCAGATGCTTCGGGAACTGCAG 135
                                                                                                                      ArgTyrMetIleLeuGlyLeuLeuAlaLeuAlaAlaValCysSerAlaAlaLysLysGly
                                                         SerSerLeuGlyGlyAspCysCysSerAspLeuGlyProGlnMetLeuArgGluLeuGln
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/note= "Derived from adenovirus
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Mismatches:
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                  The patent discloses the use of KDEL receptor inhibitor to promote secretion of proteins that are normally retained within the cell such as heat shock proteins by inhibiting KDEL receptor-mediated return of protein complexes to endoplasmic reticulum. This makes the secreted heat shock proteins more accessible to the immune system and improves immune response to a target antigen. The inhibitor protein comprises several subunits where each subunit comprises an oligomerisation domain and has at its carboxy terminus a region which binds to a KDEL receptor. The target antigen may be associated with diseases including neoplasia such as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric -
Chimeric -
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                                                                                                                                                                                                                                                                                                                                                                                                           Inhibitors of the KDEL receptor which comprises an oligomerization domain useful for promoting secretion of proteins which are normally retained within the cell .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-195296/17.
N-PSDB; AAZ50500.
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lymphoma, leukemia, with defective tumo
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                                                                                                                                                                                      oligomerisation domain; neoplasia; sarcoma; lymphoma; leukaemia; melanoma; carcinoma; glioblastoma; astromytoma; oncogene; infectious disease; allergy; autoimmune disease.
                                                                                                                Key
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Alignment Scores:
                                                                                                                 The patent discloses the use of KDEL receptor inhibitor to promote secretion of proteins that are normally retained within the cell such as heat shock proteins by inhibiting KDEL receptor-mediated return of the heat shock proteins more accessible to the immune system and improves immune response to a target antigen. The inhibitor protein comprises several subunits where each subunit comprises an oligomerisation domain and has at its carboxy terminus a region which binds to a KDEL receptor. The target antigen may be associated with diseases including neoplasia such as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and astromytoma, with defective tumour suppressor genes, oncogenes, infectious diseases, allergy or autoimmune diseases. The present sequence is KDEL receptor inhibitor protein domain from rat cartilage oligomeric matrix protein (COMP); a camel IgG linker domain
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N-PSDB;
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                                                                                     and the carboxy-terminal sequence KDEL. The subsequence GDCC is an alteration of rat COMP which provides increased stability via disulphide
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                                                                         GTCAGGGAGATCACGTTCCTGAAAAACACGGTGATGGAGTGTGACGCGTGCGGG-----
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ProAlaArgThrProGlyThrSerProGlnProGlnProLysProGlnProGlnProGlnProGln
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                 The patent discloses the use of KDEL receptor inhibitor to promote secretion of proteins that are normally retained within the cell such as heat shock proteins by inhibiting KDEL receptor-mediated return of the complexes to endoplasmic reticulum. This makes the secreted heat shock proteins more accessible to the immune system and improves immune response to a target antigen. The inhibitor protein comprises several subunits where each subunit comprises an oligomerisation domain and has at its carboxy terminus a region which binds to a KDEL receptor. The target antigen may be associated with diseases including neoplasia such as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and as tarromytoma, with defective tumour suppressor genes, oncogenes, infectious diseases, allergy or autoimmune diseases. The present sequence is KDEL receptor inhibitor comprising regions encoding a cleavable signal peptide; the oligomerisation domain of human thrombospondin 3 (TSP3) trimerisation domain, a camel IGG linker domain.
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The patent discloses the use of KDEL receptor inhibitor to promote CC secretion of proteins by inhibiting KDEL receptor-mediated return of CC heat shock proteins by inhibiting KDEL receptor-mediated return of CC protein complexes to endoplasmic reticulum. This makes the secreted heat shock proteins more accessible to the immune system and improves immune CC response to a target antigen. The inhibitor protein comprises several CC subunits where each subunit comprises an oligomerisation domain and has CC at its carboxy terminus a region which binds to a KDEL receptor. The CC target antigen may be associated with diseases including neoplasia such CC as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and CC astromytoma, with defective tumour suppressor genes, oncogenes, CC infectious diseases, allergy or autoimmune diseases. The present CC sequence is KDEL receptor inhibitor protein comprising regions including a cleavable signal peptide; the oligomerisation domain and the CC cartilage oligomeric matrix protein; a camel IgG linker domain and the

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                                                                                                                                                                                                                                                                                                                                          Chimeric
Chimeric
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       WC/200006729-A1
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                                                 "Camel IgG linker domain"
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N-PSDB; AAZ50496.
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Matches:
Conservative:
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Gaps: Mismatches: Indels:

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The patent discloses the use of KDEL receptor inhibitor to promote CC secretion of proteins that are normally retained within the cell such as CC heat shock proteins by inhibiting KDEL receptor-mediated return of CC protein complexes to endoplasmic reticulum. This makes the secreted heat shock proteins more accessible to the immune system and improves immune cresponse to a target antigen. The inhibitor protein comprises several cubunits where each subunit comprises an oligomerisation domain and has at its carboxy terminus a region which binds to a KDEL receptor. The ctarget antigen may be associated with diseases including neoplasia such CC as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and astromytoma, with defective tumour suppressor genes, oncogenes, CC infectious diseases, allergy or autoimmune diseases. The present CC sequence is KDEL receptor inhibitor comprising regions encoding a CC cleavable signal peptide; the oligomerisation domain of Xenopus CC thrombospondin 4 (TSP4) trimerisation domain including an additional CC thrombospondin 4 (TSP4) trimerisation domain including an additional companies of a camel IgG linker domain and the carboxy-terminal sequence KDEL. The subsequence GDCC is an alteration of rat cartilage oligomeric matrix protein which provides increased stability via disulphide bonds.
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ProGluGlyThrGlySerSerGluLysAspGluLeu

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                                                                                     The patent discloses the use of KDEL receptor inhibitor to promote secretion of proteins by inhibiting KDEL receptor-mediated return of heat shock proteins by inhibiting KDEL receptor-mediated return of protein complexes to endoplasmic reticulum. This makes the secreted heat shock proteins more accessible to the immune system and improves immune response to a target antigen. The inhibitor protein comprises several cresponse to a target antigen. The inhibitor protein comprises several at its carboxy terminus a region which binds to a KDEL receptor. The crayet antigen may be associated with diseases including neoplasia such as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and astromytoma, with defective tumour suppressor genes, oncogenes, infectious diseases, allergy or autoimmune diseases. The present caleavable signal peptide; the oligomerisation domain of mouse thrombospondin 3 (TSP3) trimerisation domain including an additional sequence (KDEL receptor inhibitor comprising regions and additional sequence (KDEL The subsequence GDCC is an alteration of rat cartilage oligomeric contains and the carboxy-terminal sequence contains and including an additional sequence contains an alteration of rat cartilage oligomeric contains and alteration domain of mouse cartilage oligomeric contains and alteration domain sequence contains and alteration domain of mouse cartilage oligomeric contains and alteration domain of mouse cartilage oligomeric cartilage oligomeric contains and alteration domain of mouse cartilage oligomeric cartilag
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                                                                  matrix protein which provides increased stability via disulphide bonds.
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(SLOK) SLOAN KETTERING

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC The patent discloses the use of KDEL receptor inhibitor to promote CC secretion of proteins by inhibiting KDEL receptor-mediated return of CC heat shock proteins by inhibiting KDEL receptor-mediated return of CC protein complexes to endoplasmic reticulum. This makes the secreted heat Shock proteins more accessible to the immune system and improves immune CC response to a target antigen. The inhibitor protein comprises several CC subunits where each subunit comprises an oligomerisation domain and has care its carboxy terminus a region which binds to a KDEL receptor. The CC target antigen may be associated with diseases including neoplasia such CC as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and CC infectious diseases, allergy or autoimmune diseases. The present CC sequence is KDEL receptor inhibitor comprising regions encoding a CC cleavable signal peptide; the oligomerisation domain of mouse CC thrombospondin 3 (TSP3) trimerisation domain; a camel IGG linker domain CC and the carboxy-terminal sequence KDEL. The subsequence GDCC is an CC increased stability via disulphide bonds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inhibitors of the KDEL receptor which comprises an oligomerization domain useful for promoting secretion of proteins which are normally retained within the cell -
   AAY44964;
                               AAY44964 standard; Protein; 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                        MetGlyLysPheThrValValAlaAlaAlaLeuLeuLeuLeuGlyAlaVal----
                                                                                              ProGluGlyThrGlySerSerGluLysAspGluLeu
                                                                                                                                 CCGGAAGGTACCGGATCATCAGAAAAAGATGAGTTG 339
                                                                                                                                                                                                 ССССАСССБАЛЛАССССАССССАСССССАСССССАССССАЛАССССАЛАССССАЛАССССАЛА
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                                                                                                                                                                                                                                                                    GTCAGGGAGATCACGTTCCTGAAAAACACGGTGATGGAGTGTGACGCGTGCGGGCCGCAG 243
                                                                                                                                                                                                                                                                                                                                                                      ArgAlaGluGlySerSerLeuGlyGlyAspCysCysLysAlaLeu-------Val 33
                                                                                                                                                                                                                                                                                                   ThrGlnLeuThrLeuPheAsnGlnIleLeuValGluLeuArgAspAspIleArgAspGln
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345.50
74.11%
59.82%
51.41%
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Matches:
Conservative:
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Percent Similarity:
Best Local Similarity:
Query Match:

4.32e-21 304.50 60.18% 59.29% 45.31%

Mismatches: Indels: Conservative:

29 29 29

Length: Matches:

Pred. No. Alignment Scores:

US-09-696-872-24 (1-372) x AAY44964 (1-90)

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The patent discloses the use of KDEL receptor inhibitor to promote CC secretion of proteins that are normally retained within the cell such as CC heat shock proteins by inhibiting KDEL receptor-mediated return of CC heat shock proteins by inhibiting KDEL receptor-mediated return of CC protein complexes to endoplasmic reticulum. This makes the secreted heat shock proteins more accessible to the immune system and improves immune cresponse to a target antigen. The inhibitor protein comprises several combinits where each subunit comprises an oligomerisation domain and has at its carboxy terminus a region which binds to a KDEL receptor. The CC target antigen may be associated with diseases including neoplasia such cas sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and cc astromytoma, with defective tumour suppressor genes, oncogenes, confectious diseases, allergy or autoimmune diseases. The present comprone is KDEL receptor inhibitor comprising regions encoding a CC cleavable signal peptide; the oligomerisation domain of human carconnece is KDEL receptor inhibitor comprising regions encoding a CC cleavable signal peptide; the oligomerisation domain of human cc and the carboxy-terminal sequence KDEL. The subsequence GDCC is an alteration of rat cartilage oligomeric matrix protein which provides concerns to the carboxy-terminal sequence KDEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oligomerisation domain; neoplasia; sarcoma; lymphoma; leu melanoma; carcinoma; glioblastoma; astromytoma; oncogene; infectious disease; allergy; autoimmune disease.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                              Inhibitors of the KDEL receptor which comprises an oligomerization domain useful for promoting secretion of proteins which are normal retained within the cell -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 7; 87pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rothman JE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SLOK )
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RESULT 11
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N-PSDB;
New nucleic acids are described which encode a protein comprising the second and third type 1 repeats of human TSP (thrombospondin)-1, but not the TGP (transforming growth factor)-beta activation region of human TSP-1. The nucleic acid of TSP (thrombospondin)-1 containing the second and third type-1 repeats and the COMP (cartilage oligomeric matrix protein) assembly sequence (COMP/TSP-1) was produced by PCR (polymerase chain reaction). Expression of COMP/TSP-1 caused inhibition of the growth of tumours in mice models. Thus the nucleic acids and proteins may be useful for treating
                                                                                                                                                                          Nucleic acids encoding chimeric proteins such as cartilage oligomeric matrix protein (COMP)/thrombospondins (TSP)-1 and 2, useful for inhibiting angiogenesis and treating diseases such as cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSP-1; TSP-2; COMP; cartilage oligomeric matrix protein; thrombospondin; angiogenesis; tumour; treatment; cancer; arthritis; psoriasis; diabetic retinopathy; corneal graft
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                                                                                                                                                 Claim 33; Fig 4a-b; 40pp; English.
                                                                                                                                                                                                                                                                                     Lawler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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)B; AAA47734.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment
WPI; 2000-514823,
N-PSDB; AAA47735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          angiogenesis related diseases such as cancer (by reducing the rate growth and size of tumours), arthritis, psoriasis, diabetic retinopathy, corneal graft rejection, and glaucoma. They may also be used for treating human immunodeficiency virus (HTV) infection. Anti-angiogenic therapy has little toxicity, does not require the therapeutic agent to enter tumour cells or cross the blood-brain barrier, controls tumour growth independently of growth of
                                                                                                         01-FEB-2000; 2000WO-US02482
                                                                                                                                                                                                                  glaucoma.
                                                                                                                                                                                                                          thrombospondin; angiogenesis; arthritis; psoriasis; diabetic
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                                                                                  01-FEB-1999;
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                                                                                                                                                      WO200044908-A2
                                                                                                                                                                               Synthetic.
                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                  TSP-1; TSP-2; COMP; cartilage oligomeric matrix protein;
                                                                                                                                                                                                                                                                          Human COMP/TSP-2 chimeric protein
                                                                                                                                                                                                                                                                                                   08-NOV-2000
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                                      Lawler JW;
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             2000-514823/46
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                                                            ISRAEL
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262.50
75.61%
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                                                                                                                                                                                                                              diabetic
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                                                            MEDICAL
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Conservative:
Mismatches:
Indels:
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RESULT 13
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XX O8-NC
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KW throm
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                            TSP-1; TSP-2; COMP; cartilage oligomeric matrix protein; thrombospondin; angiogenesis; tumour; treatment; cancer; arthritis; psoriasis; diabetic retinopathy; corneal graft rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding chimeric proteins such as cartilage oligomeric matrix protein (COMP)/thrombospondins (TSP)-1 and 2, useful for inhibiting anglogenesis and treating diseases such as cancer
Homo sapiens
                                 grancoma.
                                                                                                                        Human
                                                                                                                                                           08-NOV-2000
                                                                                                                                                                                                                              AAB00044 standard; Protein; 757
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                                                                                                                                                                                                                                                                                                                                                    used for treating human immunodeficiency virus (HIV) infection. Anti-angiogenic therapy has little toxicity, does not require the therapeutic agent to enter tumour cells or cross the blood-brain barrier, controls tumour growth independently of growth of tumour cell heterogeneity, and does not induce drug resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding chimeric proteins such as cartilage oligomeric matrix protein (COMP)/thrombospondins (TSP)-1 and 2, useful for inhibiting angiogenesis and treating diseases such as cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure;
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154 CAGGACGTGCGGGACTGCGGCAGCAGGTCAGGGAGATCACGTTCCTGAAAAACACG
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                                                              TGTTGTTCAGACCTGGGCCCGCAGATGCTTCGGGAACTGCAGGAAACCAACGCGGCGCTG
                                                                                                                                     TTGCTCGCCCTTGCGGCAGTCTGCCAGCGCTGCCAAAAAAGGATCCAGCCTGGGTGGAGAC
                                                                                                       LeuLeuThrLeuAlaAlaLeuGlyAlaSerGlyGlnGlyGlnSerProLeuGly-----
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                                           -SerAspLeuGlyProGlnMetLeuArgGluLeuGlnGluThrAsnAlaAlaLeu
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GlnAspValArgAspTrpLeuArgGlnGlnValArgGluIleThrPheLeuLysAsnThr

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   Percent Similarity:
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02-FEB-2001; 2001US-265928P.
09-APR-2001; 2001US-282698P.
09-APR-2001; 2001US-0829472.
04-MAY-2001; 2001US-288590P.
29-MAY-2001; 2001US-294443P.
                                                                                                                                                    The invention comprises a method of detecting a breast cancer-associated transcript in a cell from a patient. The method of the invention involves contacting a biological sample from the patient with a nucleotide that hybridises to one of the 69 breast cancer-associated gene sequences shown in the specification. The method of the invention is useful in the diagnosis or prognosis of breast cancer, and for detecting genes that are up or down-regulated in breast cancer cells. Genes identified by the method of the invention can be used in diagnostic purposes and also as targets for screening for therapeutic compounds that modulate breast cancer (e.g. hormones or antibodies). Identification of genes that are over or under expressed in breast cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein attribute and biogeneral benefits.
                                                                                                                                                                                                                                                                                                                                                                                                                          Detecting a breast cancer-associated transcript in a patient's cell, useful for diagnosing breast cancer, comprises contacting a biological sample with a polymucleotide that selectively hybridizes with breast
                                                                                                                     uragnostics, therapeutics, drug development, pharmacogenetics, protein structure and biosensor development. Amino acid sequences ABJ05536 - ABJ05504 represent the proteins encoded by the 69 breast cancer-
                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 401; 414pp; English.
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development; pharmacogenetics; biosensor development.
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)B; ABT07751.
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27-JUN-2001; 2001US-301572P.
18-JUL-2001; 2001US-306501P.
25-SEP-2001; 2001US-325002P.
05-MAR-2002; 2002US-362585P.
                                                                        Breast cancer diagnosis or treatment by comparing the expression of a marker in a patient sample with that non-breast cancer sample -
                                                       Claim 1;
                                                                                                                N-PSDB;
                                                                                                                                                                                                                                                                   21-JUN-2002; 2002WO-US19669
                                                                                                                                                                                                                                                                                                         WO2003004989-A2
                                                                                                                                                                                                                                                                                                                                             Human; breast
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DB; ACC50112.
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                                                     SEQ ID 72; 128pp;
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, Myer V, Wang
GN, Pusztai L,
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g Y, Xu Y,
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The present invention describes a method for assessing whether a patient is affilicted with breast cancer. The method comprises comparing the level of expression of a marker (gene/polypeptide see ACC50076 to ACC50334 and ABR47386 to ABR47632) in a patient sample and the normal level of expression of the marker in a control non-breast cancer sample, where a

g whether a patient comparing the level

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
Search completed: August 26, 2003, 16:21:22 Job time : 61 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       significant increase in the level of expression of the marker in the patient sample and the normal level is an indication that the patient is afflicted with breast cancer. The breast cancer associated sequences from the present invention have cytostatic activities and can be used in gene therapy. The method is useful for diagnosing and treating breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                            154
                                                                                                                                        214
                                                                                 253 AAACCG 258
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                                                                                                                                                                                                                                                                             TTGCTCGCCCTTGCGGCAGTCTGCAGCGCTGCCAAAAAAGGATCCAGCCTGGGTGGAGAC 93
                                                     ArgPro 87
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                                                                                                           ValMetGluCysAspAlaCysGlyMetGlnGlnSerValArgThrGlyLeuProSerVal 85
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Result
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-Q=/cgn2 1/USPTO_spool/US09696872/runat_26082003_150544_8745/app_query.fasta_1.519
-Q=/cgn2 1/USPTO_spool/US09696872/runat_26082003_150544_8745/app_query.fasta_1.519
-DB=IBSued_patents_AA -QFMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEARSIZE=500 -MINLEN=0 -NAXLEN=2000000000
-USER=US09696872 @GCN 1 38 @runat_260802003_150544_8745 -NCPU=6 -ICPU=3
-NO MMAD -LARGEOUERY -NEG SCORES=0 -WAIT -DSEBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Listing first 45 summaries
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1: /cgn2_6/ptodata/
2: /cgn2_6/ptodata/
3: /cgn2_6/ptodata/
4: /cgn2_6/ptodata/
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Match
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
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US-09-124-671-13

US-09-124-671-11

US-09-124-671-19

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Sequence 25,
Sequence 27,
Sequence 34,
Sequence 34,
Sequence 13,
Sequence 11,
Sequence 19,
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(i)	e 22113,	o N	e 17202	Sequence 1, Appli	e 1889	e 12,	Sequence 22, Appl	34,	6	172	Sequence 2, Appli	"	ۍ ۲	4	e 87,	e 87,	87,	87,	87,	44,		44,	44,	e 44,	38,	e 38,	e 38,	e 38,	е 38,	Sequence 2, Appli	e 1,	Sequence 45, Appl

ALIGNMENTS

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                                                           US-09-696-872-24 (1-372)
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CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                              Sequence 23, Application US/09124671A
Patent No. 6160088
GENERAL INFORMATION:
APPLICANT: Rothman, James
APPLICANT: Hoe, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chimeric human COMP-KDEL
                                                                                                                                                                                                                                                                                         LENGTH: 109
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579.00
100.00%
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APPLICANT: Rothman, James
APPLICANT: Mayhew, Mark
APPLICANT: Mayhew, Mark
APPLICANT: Mos, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEO ID NOS: 42
SOFTWARE: FASTSEO for Windows Version 3.0
SEQ ID NO 29
LENGTH: 109
TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: chimeric human TSP4-KDEL
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                                             CCGCAGCCGCAGCCGCAGCCGCAGCCGAAACCGCAAACCGGAAACCGGAAGGTACC 315
                                                                                           SerPheLeuArgAsnThrIleAlaGluCysGlnAlaCysGlyProGlnProGlnProLys
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                          ProGlnProGlnProGlnProLysProGlnProLysProGluProGluGlyThr 10:
                                                                                                                           ACGTTCCTGAAAAACACGGTGATGGAGTGTGACGCGTGCGGGCCGCAGCCGCAGCCGAAA 255
                                                                                                                                                        GlnLeuAsnGlnLeuLeuGlyGluValLysAspLeuLeuArgGlnGlnValLysGluThr 61
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GGATCATCAGAAAAAGATGAGTTG 339
                                                                                                                                                                                                                     SerSerLeuGlyGlyAspCysCysGlyAspPheAsnArgGlnPheLeuGlyGlnMetThr 41
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Matches:
Conservative:
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CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 15
LENGTH: 115
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
FEATURE: INCOMMENTANCE Sequence
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             GENERAL INFORMATION:
APPLICANT: ROthman, James
APPLICANT: Mayhew, Mark
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
                                                                                          Sequence 27, Application US/09124671A Patent No. 6160088
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GENERAL INFORMATION:
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APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
APPLICANT: HOE, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
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                                                                                US-09-124-671-34
                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: ROCHMAN, James
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
                                                                                                                                 NUMBER OF SEQ ID NOS: 42
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 34
LENGTH: 134
TYPE: PRT
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CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOPTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/124,671A CURRENT FILING DATE: 1998-07-29
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                             OTHER INFORMATION: KDEL/myc
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Percent Similarity:
Best Local Similarity:
Query Match:
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APPLICANT: Rothman, James
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
CURRENT APPLICATION UNDBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 13
LENGTH: 115
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                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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ArgAlaGluGlySerSerLeuGlyGly-----
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APPLICANT: Rothman, James
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 21
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                                                                     ATGGGAAGGTACATGATTTA-----GGCTTGCTCGCCCTTGCGGCAGTCTGCAGCGCT 63
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CCGGAAGGTACCGGATCATCAGAAAAAGATGAGTTG
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                                                                                              GTCAGGGAGATCACGTTCCTGAAAAAACACGGTGATGGAGTGTGACGCGTGCGGGCCGCAG
                                                                                                                     GlyGlnIleThrGlnMetAsnGlnMetLeuGlyGluLeuArgAspValMetArgGlnGln
                                                                                                                                                                      ArgAlaGluGlySerSerLeuGlyGlyAspCysCysGlyAspValSerArgGlnLeuIle
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US-09-124-671-17
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US-09-124-671-19
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US-09-696-872-24 (1-372) x US-09-124-671-19 (1-109)
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                                                                                                                                                                            Sequence 17, Application US/09124671A Patent No. 6160088
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 31488
CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19, Application US/09124671A Patent No. 6160088 GENERAL INFORMATION:
                                                                         APPLICANT: Rothman, James
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
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APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
SOFTWARE: FastSEQ for Windows Version 3.0
                  CURRENT APPLICATION NUMBER: US/09/124,671A CURRENT FILING DATE: 1998-07-29 NUMBER OF SEQ ID NOS: 42
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ORGANISM: Artificial Sequence
FEATURE:
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PATENT NO. 616088

GENERAL INFORMATION:
APPLICANT: Rothman, James
APPLICANT: Rothman, James
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FASESEQ for Windows Version 3.0
SEQ ID NO 25
LENGTH: 90
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US-09-124-671-25
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US-09-696-872-24 (1-372) x US-09-124-671-25 (1-90)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 25, Application US/09124671A Patent No. 6160088
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: chimeric human
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Matches:
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Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-124-671-2
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US-09-091-814-46
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                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-09-124-671-2
             Sequence 46, Application US/09091814
Patent No. 6218513
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 46
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rothman, James
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
 APPLICANT: Anthony-Cahill,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/124,671A CURRENT FILING DATE: 1998-07-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 31488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 CAGCCGCAGCCGAAACCGCAGCCGCAGCCGCAGCCGAAACCGCAGCCGAAACCG
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                                                                                                                                                      21 ValArgAppTrpLeuArgGlnGlnValArgGluIleThrPheLeuLysAsnThrValMet
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                                                                                                                    GAGTGTGACGCGTGCGGG 237
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APPLICANT: Epp, Janet K
APPLICANT: Kerwin, Bruce A.
APPLICANT: Olins O., Peter
APPLICANT: Mathews J., Antony
TITLE OF INVENTION: GLOBINS CONTAINING BINDING DOI
FILE REFERENCE: BXTB2005
CURRENT APPLICATION NUMBER: US/09/091,814
CURRENT FILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 116
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 46
                                                                                                                            ; OTHER INFORMATION: ; OTHER INFORMATION: US-09-091-814-45
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 45, Application US/09091814 Patent No. 6218513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 66
TYPE: PRT
TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description
OTHER INFORMATION: domain
                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/091,814
CURRENT FILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 116
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 45
                                                                                                                                                                                                                                                                                                                APPLICANT: Anthony-Cahill, Spencer J.
APPLICANT: Epp. Janet K
APPLICANT: Exp. Janet K
APPLICANT: Kerwin, Bruce A.
APPLICANT: Mathews J., Antony
APPLICANT: Mathews J., Antony
TITLE OF INVENTION: GLOBINS CONTAINING BINDING
FILE REFERENCE: BXTB2005
                                                                                                                                                                       LENGTH: 64
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                NO ::
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Indels:
Gaps:
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Matches:
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; LENGTH: 46
; TYPE: PRT
; ORGANISM: Ratus r
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US-09-124-671-1
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PCT-US93-11725-2
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Best Local Similarity:
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CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09124671A Patent No. 6160088
GENERAL INFORMATION:
                                                                                                                                                                             Sequence 2, Application:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rothman, James
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 31488
                                                                                                  TITLE OF INVENTION: HUMAN THROM NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS: ADDRESSEE: Wolf, Greenfield,
                             STATE: M
COUNTRY:
ZIP: 022
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READABLE FORM:
TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGAAAAAACACGGTGATGGAGTGTGACGCGTGCGGGCCGCAGCCGCAGCCGAAACCG
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                                                                                                                                                                                                                                                         CysAspAlaCysGly
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                                                                                                                                                                                               Application PC/TUS9311725
                                          Massachusetts
United States
                                                                                        600 Atlantic Avenue
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211.00
95.56%
91.11%
31.40%
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                                             of America
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Matches:
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Search completed: August 26, 2003, 16:26:26
Job time : 17.5 secs
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Best Local Similarity:
Query Match:
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FILING DATE: filed herewith
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/985,296
FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: GATES, Edward R.
NAME: GATES, Edward R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: B0801/70
REFERENCE/DOCKET NUMBER: B0801/70
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 889 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 889 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: yes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM-compatible
OPERATING SYSTEM: MS-DOS Version 3.3
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                              191 nAlaCysGlyLeuGlyProAspPheProLeuProThrLysValProGlnArgLeuAlaTh 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 pValMetArgGlnGlnValLysGluThrMetPheLeuArgAsnThrIleAlaGluCysGl 191
                                                                                           251 lileCysThrAspValAspGlu-CysArg 260
                                                                                                                                                                                           231 eAspThrGluGlyGlyPheGlnCysGlyProCysProGluGlyTyrThrGlyAsnGlyVa 251
                                                                                                                                                                                                                                                                                              211 rThrThrProProLysProArgCysAspAlaThrSerCysPheArgGlyValArgCysIl 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 lSerArgGlnLeuIleGlyGlnIleThrGlnMetAsnGlnMetLeuGlyGluLeuArgAs 171
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132 GlyAlaIleGlnGluCysPheMetGln-LysSerGluAlaGlyGlnGlnThrGlyAspVa 151
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                                                                                                                                    -----TCAGAAAAAGATGAGTTGTAGG 343
                                                                                                                                                                                                                                               ------ACCGGATCA---- 321
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33.59%
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Result
No.
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-DB=PublIshed_Applications_AA -QFWT=fastan -SUFFIX=rapb -MINMATCH=0.1
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRAMS=human40.cdi -LIST=45 -DOCALIGN=200 -THR MAT=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09696872 @CGN 1 1 83 @runat_26082003_150545_8814
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-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB
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   Score
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seg length: 2000000000
                                                                                                                                            No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                  Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO9B_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO9B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/USO9B_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/USO9B_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/USO9B_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USO0B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/USO0B_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/USO0B_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/USO0B_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/USO0B_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO0B_PUB.pep:*
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Ygapop 10.0,
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Length
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Description
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1 262.5 39.1 242 10 US-09-919-603-5 Sequence 7, Appli 262.5 39.1 300 10 US-09-919-603-7 Sequence 7, Appli 262.5 39.1 757 12 US-09-919-603-3 Sequence 3, Appli 262.5 39.1 757 12 US-09-919-603-3 Sequence 41, Appli 262.5 39.1 757 12 US-10-177-293-72 Sequence 42, Appli 262.5 39.1 757 15 US-10-177-293-72 Sequence 22, Appli 262.5 39.1 757 15 US-10-154-971-22 Sequence 27, Appli 27, 140 20.1 12.5 16.9 2456 15 US-10-154-971-24 Sequence 27, Appli 17.4 28.5 10.2 24.6 15 US-10-184-644-57 Sequence 57, Appli 17.4 28.5 10.2 24.6 15 US-10-184-634-57 Sequence 57, Appli 17.4 28.5 10.2 24.6 15 US-10-184-634-57 Sequence 57, Appli 17.4 28.5 10.2 24.6 15 US-10-184-634-57 Sequence 57, Appli 17.5 16.5 15.4 12.5 16.5 15.4 12.5 US-10-184-634-57 Sequence 417, Appli 18.5 16.5 15.4 12.5 US-10-184-634-57 Sequence 417, Appli 18.5 16.5 15.4 12.5 US-10-184-752-728 Sequence 417, Appli 18.5 16.5 15.4 12.5 US-10-184-731-741 Sequence 417, Appli 18.5 16.2 28.6 12 US-10-144-731-13 Sequence 418, Appli 18.5 16.2 28.6 12 US-10-144-731-13 Sequence 418, Appli 18.5 16.2 28.6 12 US-10-144-731-13 Sequence 419, Appli 18.5 16.2 28.6 12 US-10-144-731-13 Sequence 519, Appli 18.5 16.0 3554 12 US-10-144-731-37 Sequence 519, Appli 18.5 16.0 3554 12 US-10-144-731-37 Sequence 519, Appli 18.5 16.0 3554 12 US-10-144-731-38 Sequence 617, Appli 18.5 16.0 3554 12 US-10-144-731-38 Sequence 617, Appli 18.5 16.0 3554 12 US-10-144-731-38 Sequence 617, Appli 18.5 16.0 3554 12 US-10-144-731-38 Sequence 618, Appli 18.5 16.5 16.5 1
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ALIGNMENTS

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RESULT 1

US-09-919-603-5

; Sequence 5, Application US/09919603
; Patent NO. US20020137679A1
; GENERAL INFORMATION:
APPLICANT: Lawler, John W.
ITILE OF INVENTION: COMP/TSP-1, COMP/TSP-2 and Other TSP
ITILE OF INVENTION: Chimeric Proteins
FILE REFERENCE: 144 0.1033-007
; CURRENT APPLICATION UNMBER: US/09/919,603
; CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: FCT/US00/02482
; PRIOR APPLICATION NUMBER: FCT/US00/02482
; PRIOR APPLICATION NUMBER: 60/118,053
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 242
TYPE: PRT
; ORGANIEM: Artificial Sequence
; FEATURE:
   ORGANIEM: Artificial Sequence
; FEATURE:
   ORGANIEM: Artificial Sequence
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APPLICANT: Lawler, John W.
TITLE OF INVENTION: COMP/TSP-1, COMP/TSP-2 and Oth
TITLE OF INVENTION: Chimeric Proteins
FILE REFERENCE: 1440.1033-007
CURRENT APPLICATION NUMBER: US/09/919,603
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: PCT/US00/02482
PRIOR FILING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: FOT/US00/02482
PRIOR FILING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: 60/118,053
PRIOR FILING DATE: 1999-02-01
JUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-09-919-603-7
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Best Local Similarity:
Query Match:
DB:
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Patent No. US20020137679A1
                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                           ENGTH: 300
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                                                                                             TTGCTCGCCCTTGCGGCAGTCTGCAGCGCTGCCAAAAAAGGATCCAGCCTGGGTGGAGAC 93
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                            TGTTGTTCAGACCTGGGCCCGCAGATGCTTCGGGAACTGCAGGAAACCAACGCGGCGCTG 153
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                                                              LeuLeuThrLeuAlaAlaLeuGlyAlaSerGlyGlnGlyGlnSerProLeuGly-----
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75.61%
69.51%
39.06%
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262.50
75.61%
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Matches:
Conservative:
Mismatches:
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Gaps:
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Matches:
Conservative:
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Indels:
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
US-10-301-822-41
; Sequence 41, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals,
; APPLICANT: Berger, Allison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 21
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 757
TYPE: PRT
ORGANISM: Homo sapiens
US-09-919-603-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: COMP/TSP-1, COMP/TSP-2 & TITLE OF INVENTION: Chimeric Proteins FILE REFERENCE: 1440.1033-007 CURRENT APPLICATION NUMBER: US/09/919,603 CURRENT FILING DATE: 2001-07-30 PRIOR APPLICATION NUMBER: PCT/US00/02482 PRIOR FILING DATE: 2000-02-01 PRIOR APPLICATION NUMBER: 60/118,053 PRIOR FILING DATE: 1999-02-01
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Patent No. US20020137679A1
GENERAL INFORMATION:
APPLICANT: Lawler, John W.
                                                                                                                                                                                                                         214
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                                                                                                                                                                                                               ValMetGluCysAspAlaCysGlyMetGlnGlnSerValArgThrGlyLeuProSerVal 85
                                                                                                                                                                                                                                                                                         CAGGACGTGCGGGACTGGCTGCGGCAGCAGGTCAGGGAGATCACGTTCCTGAAAAAACACG
                                                                                                                                                                                                                                                                                                                        -----SerAspLeuGlyProGlnMetLeuArgGluLeuGlnGluThrAsnAlaAlaLeu
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262.50
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APPLICANT: MONABAN, John E.
APPLICANT: MONABAN, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASS
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASS
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MPMO1-029PZRNM
CURRENT APPLICATION NUMBER: US/10/301,822
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR PILING DATE: 2001-12-10
PRIOR PILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
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Best Local Similarity:
Query Match:
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US-10-177-293-72
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US-10-301-822-41
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LENGTH: 757
TYPE: PRT
                                                         APPLICANT: Lillie, James
APPLICANT: Glatt, Karen
APPLICANT: Zhao, Xumei
APPLICANT: Gannavarpu, Me
APPLICANT: Gannavarpu, Me
APPLICANT: Kamatkar, Shub
APPLICANT: Mertens, Maure
APPLICANT: Myer, Vic
APPLICANT: Wang, Youzhen
APPLICANT: Xu, Yongyao
                                                                                                                                                                                                                                                  Sequence 72, Application US/10177293 Publication No. US20030124128A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/381,988 PRIOR FILING DATE: 2002-05-20 NUMBER OF SEQ ID NOS: 228
                   APPLICANT:
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    Wang, Youznen
Xu, Yongyao
Hoersch, Sebastian
Monahan, John
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                                                                                                                     Gannavarpu, Manjula
Kamatkar, Shubhangi
Mertens, Maureen
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Meyers, Rachel E.
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Matches:
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Percent Similarity:
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Query Match:
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SEQ ID NO 72
LENGTH: 757
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CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 60/299,887
PRIOR FILLING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: US 60/301,572
PRIOR FILLING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: US 60/306,501
PRIOR APPLICATION NUMBER: US 60/306,501
PRIOR FILLING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: US 60/325,002
PRIOR APPLICATION NUMBER: US 60/325,002
PRIOR FILLING DATE: 2001-09-25
Sequence 4, Application US/10017721

Publication No. US20030096248A1

GENERAL INFORMATION:
APPLICANT: McCarthy, Jeanette
APPLICANT: Daley, George

APPLICANT: Daley, George

APPLICANT: Bolk, Stacey

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
FILE REFERENCE: MMI-003

CURRENT APPLICANTION NUMBER: US/10/017,721

CURRENT FILING DATE: 2001-12-14
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PRIOR FILING DATE: 2002-03-05
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Mills, Gordon B.
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Indels:
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Matches:
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US-10-154-971-22; Sequence 22, Application US/10154971; Publication No. US20030088074A1; GENERAL INFORMATION:
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Best Local Similarity:
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PRIOR FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: US 60/330,248
PRIOR FILING DATE: 2001-10-17
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 961
TYPE: PRT
ORGANISM: Homo sapiens
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CLASSIFICATION DATA:

PRIOR APPLICATION NUMBER: US/08/945,244

PILING DATE: <Unknown>
APPLICATION NUMBER: PCT/EP96/01725

APPLICATION NUMBER: PCT/EP96/01725

FILING DATE: 25-APR-1996

APPLICATION NUMBER: EP 95400932.0

FILING DATE: 25-APR-1995

ATTORNEY/AGENT INFORMATION:

NAME: Gollin, Michael A.
                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/154,971
FILING DATE: 28-May-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Muyldermans, Serge
TITLE OF INVENTION: VARIABLE FRAGMENTS OF IMMUNOGLOBULINS
USE FOR THERAPEUTIC OR VETERINARY PURP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hamers, Raymond
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                                                                                                                                                                                                                                                                                                                                                                                                               STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1100 New York Avenue, N.W., Suite 300 East CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: SPENCER & FRANK
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LENGTH: 178 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID
US-10-154-971-22
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US-10-154-971-24
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Best Local Similarity:
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     INFORMATION
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                                                                                        APPLICATION NUMBER: US/08/945,244
FILING DATE: «Unknown»
APPLICATION NUMBER: PCT/EP96/01725
FILING DATE: 25-APR-1996
APPLICATION NUMBER: EP 95400932.0
FILING DATE: 25-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: GOllin, Michael A.
REGISTRATION NUMBER: 31,957
REGISTRATION NUMBER: 31,957
                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/154,971
FILING DATE: 28-May, 2002
                                                                                                                                                                                                                                                                 CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 31,957
REFERENCE/DOCKET NUMBER: GUI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-414-4000
                                                      REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
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ADDRESSEE: SPENCER & FRANK
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COUNTRY: USA
ZIP: 20005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProGluProMetGluCysGly 164
TELEPHONE: 202-414-4000
TELEFAX: 202-414-4040
N FOR SEQ ID NO: 24:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 202-414-4040
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88.89%
20.83%
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USE FOR THERAPEUTIC OR VETERINARY PURPOSES
: 29
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CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 12544
LENGTH: 578
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Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-696-872-24 (1-372) x US-10-156-761-12544 (1-578)
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Streptomyces
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CATATGCAT 366
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                                                                                                                                                                                          CCGGAACCGGAAGGTACCGGATCATCAGAAAAAGATGAGTTGTAGGCGGCCGCAGAATTC 357
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TYPE: amino acid
TOPOLOGY: linear
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Conservative:
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APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PRE
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PRE
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILTE OF INVENTION INVESE: US/10/301,822
CURRENT APPLICATION NUMBER: US/10/301,822
CURRENT FILLING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR APPLICATION NUMBER: US 60/361,988
PRIOR APPLICATION NUMBER: US 60/361,988
PRIOR APPLICATION NUMBER: US 60/361,988
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US-10-184-644-57
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Best Local Similarity:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 155
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                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     Sequence 57, Application US/10184644
Publication No. US20030044930A1
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APPLICANT:
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APPLICANT:
                APPLICANT: Zhang,Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C227
                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                        APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
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                                                                                                                                APPLICANT:
CURRENT APPLICATION NUMBER: US/10/184,644
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ORGANISM: Homo Sapiens
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                                                                                                      Watanabe, Colin K. Wood, William I.
                                                                                                                                                     Smith, Victoria
                                                                                                                                                                                               Gurney, Austin L.
                                                                                                                                                                                                                       Goddard, Audrey
Godowski, Paul
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Schlegel, Robert
Monahan, John E.
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Guillemette, Tracy L.
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; Prior Application removed -
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 57
; LENGTH: 2456
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-184-644-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
US-10-184-634-57
; Sequence 57, Application US/10184634
; Publication No. US20030068684A1
                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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 US-09-696-872-24
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul (
APPLICANT: Gurney, Austin 1
                                                                                                                                                                                                                         Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 57
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APPLICANT:
APPLICANT:
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                                                                                                                                                                        LENGTH: 2456
TYPE: DNA
ORGANISM: Homo S
                                                                                                                                                                                                                                                                    TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C217
CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT FILING DATE: 2002-06-28
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Godowski, Paul J.
Gurney, Austin L.
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 (1-372)
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US-10-280-953-17
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Pred. No.:
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                                                                                                                           Sequence 17, Application US/10280953 Publication No. US20030113317A1 GENERAL INFORMATION:
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SEQ ID NO 228
LENGTH: 285
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 APPLICANT: Yue, Henry
APPLICANT: Arvizu, Chandra S.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: MOLECULE ASSOCIATED WITH
FILE REFERENCE: PC-0018-1 CIP
FILE REFERENCE: TC-0018-1 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/881,752A CURRENT FILING DATE: 2001-06-15 PRIOR APPLICATION NUMBER: US 08/833,457 PRIOR FILING DATE: 1997-04-01 NUMBER OF SEQ ID NOS: 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Tomb, Jean-Francois
APPLICANT: Oomen, Raymond P.
TITLE OF INVENTION: Identification of Polynucleotides
TITLE OF INVENTION: Encoding No. US20020115078A1el Helicobacter Polypeptides in
TITLE OF INVENTION: Genome
FILE REFERENCE: 06132/041002
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ORGANISM: Helicobacter
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APPLICATION NUMBER:
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US/10/280,953
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CURRENT FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 09/602,565
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/106,920
; PRIOR FILING DATE: 1998-06-29
; NUMBER OF SEQ ID NOS: 17
; SOFTMARE: PERL Program
; SEQ ID NO 17
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Mus musculus
; PEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID NO. US200
US-10-280-953-17
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                               Alignment Scores:
Pred. No.:
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US-10-140-472-417
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US-10-140-472-417
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NUMBER OF SEQ ID. NOS: 550
SEQ ID NO 417
LENGTH: 1547
TYPE: DNA
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CURRENT FILING DATE: 2002-05-06
                                                                                                                                                                                                              APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C168
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Godowski, Paul J.
Gurney, Austin L.
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Wood, William
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time: 46.5 secs
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                                                                780 AlaGlyThrThrCysThrGlyGlyCysGly 789
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-Q=/Cgn2_1/USPTO_spool/US09696872/runat_26082003_150543_8735/app_query.fasta_1.519
-DB=PIR_76_-QFMT=fastan_-SUFFIX=xpr_-MINMATCH=0.1_-LOOPEL=0_-LOOPEXT=0_-UNITS=bits_START=1_-END=-1_-MATRIX=blosum62_-TRANS=human40.cdi_-LIST=45_-DCALIGN=200_-THR_SCORE=pct_-THR_MAX=100_-THR_MIN=0_-ALIGN=15_-MODE=LOCAL_-OUTFMT=ptc_0_-NONME=xt_-HEAPSIZE=550_-MINLEN=0_-MAXIEN=200000000_-USER=US09696872_@CGN_1_1_62_@runat_26082003_150543_8735_-NCPU=6_-ICPU=3_-NO_MMAD_-LARGEQTERY_-NEG_SCORES=0_-MAIT_-DSPBLOCK=100_-LONGLOG_-DEV_TIMEDUT=30_-THREADS=1_-XGAPEXT=0_-S-FGAPOP=6_-DEV_TIMEDUT=30_-THREADS=1_-XGAPOP=10_-XGAPEXT=0_.5_-FGAPOP=6_-PGAPEXT=7_-YGAPOP=10_-YGAPEXT=0_.5_-DELOP=6_-DELEXT=7_-
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-MODEL=frame+_n2p.model
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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seq length: 2000000000
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2: pir2:
3: pir3:
4: pir4:
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Ygapop 10.0 , X
Fgapop 6.0 , I
Delop 6.0 , I
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A45441
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myelin regulatory
PO-rich protein -
procyclic acidic r
hypothetical prote
glycine tyrosine-r
proline-rich prote
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ALIGNMENTS

Percent Similarity:
Best Local Similarity:
Query Match:
DB: C;Keywords: pentamer F;1-19/Domain: signal sequence #status predicted <SIG> F;182-219/Domain: EGF homology <EGF> R;Oldberg, A.; Antonsson, P.; Lindblom, K.; Heinegard, D.
J. Biol. Chem. 267, 22346-22350, 1992
A;Title: COMP (cartilage oligomeric matrix protein) is structurally related to the thromt A;Reference number: A44315; MUID:93054522; PMID:1429587
A;Accession: A44315
A;Molecule type: mRNA
A;Residues: 1-755 <OLD> 밁 Ś A;Cross-references: GB:X72914; NID:g297438; PIDN:CAA51419.1; PID:g297439 A;Experimental source: tracheal chondrocyte A;Note: sequence extracted from NCBI backbone (NCBIP:117022) C;Superfamily: thrombospondin 3; EGF homology N;Alternate names: thrombospondin homolog COMP C;Species: Rattus norvegicus (Norway rat) S C;Date: 30-Apr-1993 #sequence_revision 03-May-1994 #text_change 02-Aug-2002 C;Accession: A44315 US-09-696-872-24 (1-372) x A44315 (1-755) Score: Pred. No.: Alignment Scores: cartilage oligomeric matrix protein precursor - rat A44315 TGTTGTTCAGACCTGGGCCCGCAGATGCTTCGGGAACTGCAGGAAACCAACGCGGCGCTG TTGCTCGCCCTTGCGGCAGTCTGCAGCGCTGCCAAAAAAAGGATCCAGCCTGGGTGGAGAC ValLeuAlaLeuAlaAlaLeuArgAlaThrGlyGlnGlyGlnIleProLeuGlyGly---6.48e-13 234.00 72.84% 62.96% 34.82% Conservative: Mismatches: Indels: Length: Matches: 755 51 8 18 153 27 93

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A; Residues: 1-955 < LAW>
A; Residues: 1-955 < LAW>
A; Cross-references: GB: Z19091; NID: g288777; PIDN: CAA79518.1; PID: g288778
A; Note: sequence extracted from NCBI backbone (NCBIN: 124858, NCBIP: 124860)
C; Superfamily: thrombospondin 3; EGF homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Lawler, J.; Duquette, M.; Whittaker, C.A.; Adams, J.C.; McHenry, K.; DeSimone, D.W. J. Cell Biol. 120, 1059-1067, 1993
A;Title: Identification and characterization of thrombospondin-4, a new member of the A;Reference number: A45441; MUID:93163109; PMID:8432726
A;Accession: A45441
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C;Species: Xenopus laevis (African clawed frog)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
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                                           lileCysThrAspValAspGlu-CysArg 326
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                                                                                                      eAspThrGluGlyGlyPheGlnCysGlyProCysProGluGlyTyrThrGlyAsnGlyVa
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146.50
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33.59%
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4.04e-05
145.50
57.14%
42.86%
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Ig gamma-2 chain - Arabian camel (fragment)
C;Species: Camelus dromedarius (Arabian camel)
C;Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 11-Ja:
C;Accession: S33598
R;Hamers-Casterman, C; Atarhouch, T:; Muyldermans, S:; Robinson, G:;
Nature 363, 446-448, 1993
A;Title: Naturally occurring antibodies devoid of light chains.
A;Reference number: S33598; MUID:93275410; PMID:8502296
A;Accession: S33598
A;Accession: S3598
A;Acc
C;Keywords: beta-hydroxyasparagine; beta-hydroxyaspartic acid; calcium binding; F;1-21/Domain: signal sequence #status predicted <SIG>F;22-961/Product: thrombospondin 4 #status predicted <MAT>F;290-324/Domain: EGF homology <EGF1>F;330-362/Domain: EGF homology <EGF>F;330-362/Domain: EGF homology <EGF-F;562-564/Region: cell attachment (R-C-D) motif F;303/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted F;343/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted F;612,941/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Molecule type: mRNA
A;Residues: 1-961 <LAW>
A;Residues: 1-961 <LAW>
A;Cross references: EMBL:Z19585; NID:g311625; PIDN:CAA79635.
A;Cross references: translated the codon GTG for residue 616 as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GDB:463011; OMIM:600715
A;Map position: 1q21-1q23
C;Complex: homotrimer, disulfide linked
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Lawler, J.; McHenry, K.; Duquette, M.; Derick, L. J. Biol. Chem. 270, 2809-2814, 1995
A;Title: Characterization of human thrombospondin-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 11-Aug-1995 #text_change 13-Aug-1999
C;Accession: A55710; S36069
                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Description: participates in cell migration and adhesion, and in platelet aggregation C;Superfamily: thrombospondin 3; EGF homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: A55710; MUID:95155352; PMID:7852353 A;Accession: A55710
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Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
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Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIDN:CAA79635.1; PID:G311626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135
25
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Length:
Matches:
Conservative:
Mismatches:

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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-26, 'I',28-68, 'PMLRR',75-126, 'P',128-134, 'PPPNANDP',135-332 <
A;Residues: 1-26, 'I',28-68, 'NID:g160245; PIDN:AAA29577.1; PID:g160246
A;Cross-references: GB:M14135; NID:g160245; PIDN:AAA29577.1; PID:g160246
R;Weber, J.L.; Egan, J.E.; Lyon, J.A.; Wirtz, R.A.; Charoenvit, Y.; Maloy, Exp. Parasitol. 63, 295-300, 1987
Exp. Parasitol. 63, 295-300, 1987
A;Title: Plasmodium berghei: cloning of the circumsporozoite protein gene.
A;Reference number: S13446; MUID:87218962; PMID:3556207
A;Accession: S13446
                                                                                                                                                                                                                                                                                                  C;Comment: There are three distinct regions in the mature circumsporozoite protobic membrane-anchoring sequence
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
C;Keywords: sporozoite; surface antigen; tandem repeat
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-33/Product: circumsporozoite protein #status predicted <MAT>
F;24-189/Region: 8-residue repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Status: preliminary
A,Molecule type: DNA
A,Residues: 61-122,'A',124-332 <WEB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:M28887
R;Eichinger, D.J.; Arnot, D.E.; Tam, J.P.; Nussenzweig, V.; Enea, V.
Mol. Cell. Biol. 6, 3965-3972, 1986
A;Title: Circumsporozoite protein of Plasmodium berghei: gene cloning and A;Reference number: A25083; MUID:87089740; PMID:2432395
A;Accession: A25083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N;Alternate names: sporozoite surface antigen
C;Species: Plasmodium beprehei
C;Date: 30-Sep-1987 #sequence revision 28-Jul-1995 #text_change 16-Jul-1999
C;Accession: A44948; A25083; $13446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Sequence of the circumsporozoite gene of Plasmodium berghei ANKA clone and NK6 A;Reference number: A44948; MUID:90158693; PMID:2406593 A;Accession: A44948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
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DB:
                                                                                                                                                                                                    Alignment
                                                                                                                                                                                                                                                       F;258-310/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:M25445; NID:g160177; PIDN:AAA29531.1; PID:g160178 C;Comment: There are three distinct regions in the mature circumsporozoite protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     circumsporozoite protein precursor - Plasmodium berghei (strain NK65)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
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US-09-696-872-24
                                                  Query Match:
DB:
                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nar, D.E.
Biochem. Parasitol. 39, 151-154, 1990
                                                                                                                                                                               No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-332 <LAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LysAspLeuLeuArgGlnGlnValLysGluThrSerPheLeuArgAsnThrIleAlaGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AlaPro---ProAlaProProThrArgPro 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGCCGCAGCCGAAACCGCAGCCGAAACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CysGlnAlaCysGlyProLeuLysPheGlnSerProThrProSerThrValValAlaPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTGACGCGTGCGGGCCG------CAGCCGCAGCCGAAACCGCAGCCGCAGCCG 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGGGACTGGCTGCGGCAGCAGGTCAGGGAGATCACGTTCCTGAAAAACACGGTGATGGAG 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AspPheAsnArgGlnPheLeuGlyGlnMetThrGlnLeuAsnGlnLeuLeuGlyGluVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GACCTGGGCCCGCAGATGCTTCGGGAACTGCAGGAAACCAACGCGGCGCTGCAGGACGTG 162
(1-372)
                                                                                                                                                                                                                                                    thrombospondin
                                                                                                                                                                                                                                                                               2-residue repeats
                                                                       0.000613
133.00
87.50%
62.50%
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OZZQMB
                                                                                                                                                                                                                                                    type 1 repeat homology <THR1>
(1-332)
                                                                             Mismatches
Indels:
                                                                                                                       Conservative:
                                                                                                                                                     Matches:
                                               0 4 8 2 3 3 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hockmey
                                                                                                     A;FUCUEOCH, D.J.; Dalrymple, M.A.; Davison, A.J.; Dolan, A.; Frame, M.C.; McNab, J. Gen. Virol. 69, 1531-1574, 1988
A;Title: The complete DNA sequence of the long unique region in the genome of he A;Reference number: A30083; MUID:88274327; PMID:2839594
A;Stature: The complete DNA sequence of the long unique region in the genome of he A;Recession: I30085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Lookyer, M.J.
submitted to the EMBL Data Library, November 1989
A;Reference number: S12571
A;Accession: S12571
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A;Cross-references: EMBL:X17606; NID:g9784; PIDN:CAA35608.1; PID:g9785
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
C;Keywords: tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Nucleotide sequence of the Plasmodium berghei circumsporozoite protein gene from A;Reference number: S07873; MUID:90221834; PMID:2183186 A;Accession: S07873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change C;Accession: 807873; S12571 R;Lockyer, M.J.; Davies, C.S.; Suhrbier, A.; Sinden, R.E. Nucleic Acids Res. 18, 376, 1990
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                  A;Cross-references: GB:X14112; NID:g1944536; PIDN:CAA32311.1; PID:g59536; GB:D00317
                                               A; Residues: 1-3164 < MCG:
                                                                     A; Molecule type: DNA
                                                                                                  A;Status: nucleic
                                                                                                                                                                                                                                                                                                                          UL36 protein - human herpesvirus 1 (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-696-872-24 (1-372) x OZZQBK (1-348)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
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A; Residues: 1-59,'I',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-348 <LOC>
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                                                                                                                                                                                                                                                          ;Species: human herpesvirus 1
;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 16-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;1-20/Domain: signal sequence #status predicted <SIG>;21-348/product: circumsporozoite protein #status pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                    245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCGGAACCGGAAGGTACCGGATCATCAGAAAAAGAT 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCGCAGCCGCAGCCGAAACCGCAGCCGCAGCCGCAGCCGAAACCGCAGCCGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCGGAACCGGAAGGTACCGGATCATCAGAAAAAAGAT 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProGlnProGlnProGlnProGlnProGlnProGlnProArgProGlnProGln
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                                                                                             acid sequence
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133.00
87.50%
62.50%
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                                                                                               shown;
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e antigen
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Matches:
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Indels:
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                                                                                               translation
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D.; Perry

S В S

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RESULT 9
A55335
myelin regulatory factor 1 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #te
C;Accession: A55335
R;Haque, N.S.; Buchberg, A.M.; Khalili, K.
J. Biol. Chem. 269, 31149-31156, 1994
A;Title: Isolation and characterization of MRF-1, a br
A;Reference number: A55335; MUID:95074156; PMID:752704
A;Accession: A55335
A;Status: preliminary
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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C;Function
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Best Local Similarity:
Query Match:
DB:
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C; Keywords: phosphoric
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A;Residues: 1-1494 <CAO>
A;Cross-references: EMBL:AF077000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: A novel putative protein-tyrosine A;Reference number: Z18004; MUID:98361981; A;Accession: T14355
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                                                                                                                                                                                                                                                            CCGGAACCGGAA 309
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S58222
PQ-rich protein - human
C;Species: Homo sapiens (man)
C;Species: 13-Jan-1996 #sequence_revision 01
C;Date: 13-Jan-1996 #sequence
C;Accession: S58222
R;Wagner, F.F.; Flegel, W.A.
submitted to the EMBL Data Library, July
A;Description: A CDNA, which predicts a p
A;Reference number: S58222
A;Accession: S58222
A;Accession: S58222
A;Accession: S58222
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A;Molecule type: mRNA
A;Residues: 1-400 <WAG>
A;Cross-references: EMBJ
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A;Cross-references: GB:U14648
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| SerProArgArgProAlaAlaAlaIleSerLysProGlu---
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A;Cross-references: GB:X04814; NID:g10510; PIDN:CAA28503.1; PID:g10511
R;Vijayasarathy, S.; Ernest, I.; Itzhaki, J.; Sherman, D.; Mowatt, M.R.; Michels, P.A.N.
submitted to the EMBL Data Library, April 1990
A;Description: The genes encoding fructose bisphosphate aldolase in trypanosoma brucei
A;Reference number: S21538
A;Accession: S21540
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Nature 325, 272-274, 1987
                                                                                                                                                                                                                   R; Lennard, N.
submitted to the EMBL Data Library, November 1995
A; Reference number: Z19895
A; Accession: T24470
                                                                                                                                                                                                                                                                                                    hypothetical protein T04F8.8 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000 C;Accession: T24470
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Alignment Scores:
                                       A; Introns: 18/2; 63/1
                                                              A; Map position: X
                                                                              A; Gene: CESP: T04F8.8
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A; Residues: 1-165 < W
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A; Residues: 1-129 < VIJ>
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A; Residues: 1-129 < ROD>
                                                                                                                        A; Experimental source:
                                                                                                                                      A;Cross-references: EMBL:Z66565; PIDN:CAA91483.1; GSPDB:GN00028; CESP:T04F8
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proline-rich protein - wheat
c;Specles: Triticum aestivum
c;Date: 20-Feb-195 #sequence_revision 20-F
C;Accession: S14959
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A;Accession: T17638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glycine tyrosine-rich protein a147L - Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-260 <GRA>
A;Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96515.1
A;Experimental source: specific host Chlorella strain NC64A
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Best Local Similarity:
R; Raines, C.A.; Lloyd, J.C.; Chao, Plant Mol. Biol. 16, 663-670, 1991
                                                                                                                                                                                                                                                                            US-09-696-872-24 (1-372) x T17638 (1-260)
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R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Higasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7:
A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: C91067
A;Accession: C91067
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-422 <HAY>
A;Residues: 1-422 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB36930.1; PID:g13362978; GSPDB:GN00154
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(291067)
hypothetical protein ECs3507 [imported] - Escherichia coli (strain O157:H7, hypothetical protein ECs3507 [imported] - Escherichia coli (strain O157:H7, C;Species: Escherichia coli (strain O157:H7, C;Species: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 C;Accession: C91067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-378 <RAI>
A;Cross-references: EMBL:X52472; NID:g21841; PIDN:CAA36712.1;
C;Superfamily: hydroxyproline-rich glycoprotein
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A;Reference number: S14959; MUID:91329699; PMID:1714320
A;Accession: S14959
A;Status: preliminary
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Best Local Similarity:
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
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                     CCGGAACCGGAAGGTACCGGATCATCAGAAAAAGAT 333
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ProGluProGluProIleArgSerSerLeuLysGlu 398
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Search completed: August 26, 2003, 16:25:51 Job time : 33.5 secs

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-MODEL-frame+ n2p.model -DEV=xlp
-Q=/cgn2 1/USFTO_spool/US90696872/runat_26082003_150542_8719/app_query.fasta_1.519
-Q=/cgn2 1/USFTO_spool/US90696872/runat_26082003_150542_8719/app_query.fasta_1.519
-DB=SwissFrot_41 -QFMT=fastan -SUFFIX=rsp -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09696872_9CGN_1 1_30 @runat_26082003_150542_8719 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSFBLOCK=T00 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
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Maximum DB seq length: 200000000
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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ALIGNMENTS

RA R	RA R	REAL SECTION OF SECTIO
VARIANTS MED TYR-342, AND VARIANT PSACH ARG-328. MEDLINE=95400302; PubMed=7670472; Briggs M.D., Hoffman S.M.G., King L.M., Olsen A.S., Mohrenweiser H., Leroy J.G., Mortier G.R., Rimoin D.L., Lachman R.S., Gaines E.S., Cekleniak J.A., Knowlton R.G., Cohn D.H.; "Pseudoachondroplasia and multiple epiphyseal dysplasia due to mutations in the cartilage oligomeric matrix protein gene."; Nat. Genet. 10:330-336(1995). [4] VARIANT MED LYS-523.	Newton G., Weremowicz S., Morton C.C., Copeland N.G., Gilbert D.J., Jenkins N.A., Lawler J.; "Characterization of human and mouse cartilage oligomeric matrix protein."; Genomics 24:435-439(1994). [2] VARIANTS PSACH SER-459 DEL; TYR-468 AND TYR-472. MEDLINE=95400301; PubMed=7670471; Hecht J.T., Nelson L.D., Crowder E., Wang Y., Elder F.F.B., Harrison W.R., Francomano C.A., Prange C.K., Lennon G.G., Deere M., Lawler J.; "Mutations in exon 17B of cartilage oligomeric matrix protein (COMP) cause pseudoachondroplasia."; Nat. Genet. 10:325-329(1995).	COMP_HUMAN STANDARD; PRT; 757 AA. COMP_HUMAN STANDARD; PRT; 757 AA. AC P49747; Q16388; Q16389; DT 01-CCT-1996 (Rel. 34, Created) DT 01-CCT-1996 (Rel. 34, Last sequence update) DT 02-FEB-2003 (Rel. 41, Last sequence update) DE Cartilage oligomeric matrix protein precursor (COMP). COMP. COMP. OS Homo sapiens (Human). OS Homo sapiens (Human). OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. OX NCBI_TaxID=9606; RN [1] RP SEQUENCE FROM N.A. RC TISSUE=Cartilage; Physhed=7711493:

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Pseudoachondroplasia due to the substitution of the highly conserved RT Asp482 by Gly in the seventh calmodulin-like repeat of cartilage RT Asp482 by Gly in the seventh calmodulin-like repeat of cartilage RT Asp482 by Gly in the seventh calmodulin-like repeat of cartilage RT oligomeric matrix protein.",

RT Hum. Mutat. Suppl. 1:S125-S127(1998).

CC -!- SUBUNIT: PENTAMER; DISULFIDE-LINKED.

CC -!- SUBGRASE: DEFECTS: IN COMP ARE THE CAUSE OF PSEUDOACHONDROPLASIA CC (PSACH) AND MULTIPLE EPIPHYSEAL DYSPLASIA (MED OR EDM1), WHICH ARE CC (PSACH) AND MULTIPLE EPIPHYSEAL DYSPLASIA (MED OR EDM1), WHICH ARE CC (PSACH) AND MULTIPLE EPIPHYSEAL DYSPLASIA (MED OR EDM1), WHICH ARE CC (PSACH) AND MULTIPLE EPIPHYSEAL DYSPLASIA (MED OR EDM1), WHICH ARE CC (TATURE AND EARLY-ONSET OSTEOARTHROSIS. HEADLY CATEGORIZED BY SHORT CC (INTO THE MORE SEVERE FAIRBANK AND THE MILDER RIBBING TYPES. PSACH IS MORE SEVERE AND IS RECOGNIZED IN EARLY CHILDHOOD.

CC --- SIMILARITY: Contains 4 EGF-like domains.

CC --- SIMILARITY: Contains 7 TSP type-3 domains.
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                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-99118868; PubMed-9921895; Ikegawa S., Ohashi H., Nishimura G., Kim K.C., Sannohe A., Kimtzuka M., Fukushima Y., Nagai T., Nakamura Y.; "Novel and recurrent COMP (cartilage oligomeric matrix protein) mutations in pseudoachondroplasia and multiple epiphyseal dysplasia."; hum. Genet. 103:633-638(1998).
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EMBL; L32137; AAA57253.1; -.
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Loughlin J., Irven C., Mustafa Z., Briggs M.D., Carr A., Lynch &
Knowlton R.G., Cohn D.H., Sykes B.;
"Identification of five novel mutations in cartilage oligomeric
"matrix protein gene in pseudoachondroplasia and multiple epiphys
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Susic S., McGrory J., Ahier J., Cole W.G.;
"Multiple epiphyseal dysplasia and pseudoachondroplasia due to novel
mutations in the calmodulin-like repeats of cartilage oligomeric
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Ballo R., Briggs M.D., Cohn D.H.,
Ramesar R.S.;
"Multiple epiphyseal dysplasia, ri
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A., Leroy J.G., Biesecker
Rimoin D.L., Knowlton R.G.
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Pfam; PF02412; tsp_3; 11.

SMART; SM00179; EGF CA; 2.

PROSITE; PS00022; EGF 1; FALSE_NEG.

PROSITE; PS01186; EGF_2; 1.

PROSITE; PS01187; EGF_CA; 2.
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G-> R (IN PSACH; MILD FORM).

(FTId=VAR 007615.

C-> R (IN PSACH; MILD FORM).

(FTId=VAR 007616.

D-> Y (IN MED; FAIRBANK TYPE)

(FTId=VAR 007617.

D-> V (IN PSACH; MILD FORM).

(FTId=VAR 007618.

D-> V (IN MED; FAIRBANK TYPE)

(FTId=VAR 007619.
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EGF-LIKE 2,
EGF-LIKE 4.
TSP TYPE-3
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CELL ATTACHMENT SITE (POTENTIAL)
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                                                                                                                                     TISSUE=Cartilage;
MEDLINE=93054522; PubMed=1429587;
Oldberg A., Antonsson P., Lindblom K., Heinegaard D.;
"COMP (cartilage oligomeric matrix protein) is structuto the thrombospondins.";
J. Biol. Chem. 267:22346-22350(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMP_RAT
P35444;
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01-JUN-1994 (Rel. 29, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Cartilage oligomeric matrix protein precursor (COMP).
Engel J.;
"The crystal structure c
prototype ion channel?";
                                                               X-RAY CRYSTALLOGRAPHY (2.05 ANGSTROMS)
MEDLINE=97020114; PubMed=8864111;
Malashkevich V.N., Kammerer R.A., Efim
                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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/FIId=VAR 007624.
C -> G (ĪN PSACH; MILD FORM) .
/FIId=VAR 007625.
/FIId=VAR 007626.
/FIId=VAR 007626.
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d=VAR 007621.

S (IN MED; FAIRBANK TYPE).

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                                                          Efimov V.P., Schulthess T.,
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InterPro; IPR001881; EX
InterPro; IPR006209; EX
InterPro; IPR003367; t:
Pfam; PF000008; EGF; 1.
Pfam; PF02412; tsp 3;
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
entitles requires a license agreement (See http://www.isb-
or send an email to license@isb-sib.ch).
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PDB; 1VDF; 08-OCT-97.
PDB; 1FBM; 09-AUG-00.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                     member of the thrombospondin gene family.";

J. Cell Biol. 120:1059-1067 (1993).

-I- FUNCTION: ADHESIVE GLYCOPOTEIN THAT MEDIATES CELL-TO-CELL AND CELL-TO-MATRIX INTERACTIONS. CAN BIND TO FIBRINOGEN, FIBRONECTIN, LAMININ AND TYPE V COLLAGEN. MAY PARTICIPATE IN THE GENESIS AND FUNCTION OF CARDIAC AND SKELETAL MUSCLE.

-I- SUBUNIT: Homocrimer; disulfide-linked.

-I- DEVELOPMENTAL STAGE: INITIAL EXPRESSION DURING NEURULATION.
INCREASE DURING TAILBUD STAGES BUT DECREASE BY THE FEEDING TADPOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thrombospondin 4 precursor.

Thrombospondin 4 precursor.

Renopus laevis (African clawed frog).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota, Metazoa; Chordata; Craniata; Pipoidea; Pipidae;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lawler J., Duquette Desimone D.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=93163109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q06441;
01-JUN-1994 (Rel. 29,
01-JUN-1994 (Rel. 29,
28-FEB-2003 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lawler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Identification and characterization of thrombospondin-4, a

⟨enopodinae; Xenopus.
                                                                                                                                                                                                                                        STAGE.

SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.

SIMILARITY: Contains 4 EGF-like domains.

SIMILARITY: Contains 7 TSP type-3 domains.

SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
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te M., Whittaker C.A.,
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Matches:
Conservative:
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GlyAlaIleGlnGluCysPheMetGln-LysSerGluAlaGlyGlnGlnThrGlyAspVa GGCAGTCTGCAGCGCTGCCAAAAAAGGATCCAGCCTGGGTGGAGACTGTTGTTCAGACCT 107

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US-09-696-872-24 (1-372)
                             Query Match:
                                        Percent Similarity:
Best Local Similarity:
                                                            Score:
                                                                                                  InterPro; IPR001881; I
InterPro; IPR006209; I
InterPro; IPR003367; I
InterPro; IPR003129;
                                                                                                           DISULFID
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Pram; Pr02412; tsp 3; 9.

Pram; Pr02210; TSPN; 1.

SMART; SM00179; EGF CA; 2.

SMART; SM00210; TSPN; 1.

PROSITE; PS00126; EGF; 1; FALSE_NEG.

PROSITE; PS01186; EGF CA; 2.

PROSITE; PS01187; EGF_CA; 2.

Glycoprotein; Cell adhesion; Calcium-binding; Repeat; EGF-like domain;
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EGF_like.
tsp_3.
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TSP4_XENLA
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INTERCHAIN (PROBABLE)
BY SIMILARITY.
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EGF-LIKE 1.
EGF-LIKE 2,
EGF-LIKE 3,
EGF-LIKE 4.
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 (1-955)
                  Length:
Matches:
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Mismatches:
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01-JUN-1994
01-JUN-1994
28-FEB-2003
                                                                Genew;
GO; GO;
GO; GO;
GO; GO
                                                                                                                                                                       EMBL; Z19585; CAA79635.1;
PIR; A55710; TSHUP4.
HSSP; P35444; 1VDF.
Genew; HGNC:11788; THBS4.
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the Euro
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P35443;
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HUMAN
                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not remove entities requires a license agreement (so or send an email to license@isb-sib.ch)
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Lawler J., Duquette M., Urry L., McHenry K., Smith T.F.;
Lawler J., Duquette M., Urry L., McHenry K., Smith T.F.;
"The evolution of the thrombospondin gene family.";
J. Mol. Evol. 36:509-516(1993).
-!- FUNCTION: ADHESIVE GLYCOPROTEIN THAT MEDIATES CELL-TO-CELL AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CELL-TO-MATRIX INTERACTIONS. CAN BIND TO FIBRINGEN, LAWININ AND TYPE V COLLAGEN.
SUBUNIT: Homotrimer; disulfide-linked.
SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.
SIMILARITY: Contains 4 EGF-like domains.
SIMILARITY: Contains 7 TSP type-3 domains.
SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
                                                            ; 600715; -.
GO:0005578; C:extracellular matrix; TAS.
GO:0005509; F:calcium ion binding activity;
GO:0008201; F:heparin binding activity; TAS.
GO:0006930; P:substrate-bound cell migration
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IPR001881; EGF_Ca.
IPR006209; EGF_like.
IPR003367; tsp_3.
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(Rel. 29,
(Rel. 41,
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                                                                  migration,
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                                                                                                             TAS.
                                                                  cell
                                                                  extension;
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Pfam; PF000008; EGF; 2.
Pfam; PF02412; t5p_3; 9.
Pfam; PF02210; TSPN; 1.
SMART; SM00179; EGF CA; 2.
SMART; SM00210; TSPN; 1.
PROSITE; PS001022; EGF 1; FAI
PROSITE; PS001186; EGF 2; 1.
PROSITE; PS01187; EGF CA; 2.
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    TGTGACGCGTGCGGGCCG--
                                                                     AspPheAsnArgGlnPheLeuGlyGlnMetThrGlnLeuAsnGlnLeuLeuGlyGluVal
                                                                                                                                                                       GACCTGGGCCCGCAGATGCTTCGGGAAACTGCAGGAAACCCAACGCGGCGCTGCAGGACGTG
                                          LysAspLeuLeuArgGlnGlnValLysGluThrSerPheLeuArgAsnThrIleAlaGlu
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145.50
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42.86%
21.65%
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BY SIMILARITY.
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EGF-LIKE 2, CALCI
EGF-LIKE 3, CALCI
EGF-LIKE 4.
TSP TYPE-3 1.
TSP TYPE-3 2.
TSP TYPE-3 3.
TSP TYPE-3 5.
TSP TYPE-3 5.
TSP TYPE-3 6.
TSP TYPE-3 6.
TSP TYPE-3 7.
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CELL ATTACHMENT S
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THROMBOS PONDIN
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                                                                                                                                                                                                                 (1-961)
                                                                                                                                                                                                                                                                             Conservative: Mismatches: Indels:
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Matches:
                                                                                                                                                                                                                                                           Gaps:
    - CAGCCGCAGCCGAAACCGCAGCCGCAGCCG
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Pfam; PF00008; EGF; 2.
Pfam; PF02410; tsp; 3; 9.
Pfam; PF02410; TSPN; 1.
SMART; SM00179; EGF CA; 2.
SMART; SM00210; TSPN; 1.
SMART; SM00210; TSPN; 1.
PROSITE; PS001022; EGF 1; FALSE NEG.
PROSITE; PS01187; EGF 2; 1.
PROSITE; PS01187; EGF CA; 2.
                                                                                                                                                                          Glycoprotein;
Signal
Signal
SIGNAL
CHAIN
DOMAIN
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P49744;
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-i- FUNCTION: ADHESIVE GLYCOPROTEIN THAT MEDIATES CELL-TO-CELL AND CELL-TO-MATRIX INTERACTIONS. CAN BIND TO FIBRINOGEN, FIBRONECT!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata;
Mammalia, Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <del>:</del>
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STRAIN=Lewis; TISSUE=Skeletal muscle;
MEDLINE=96074771; PubMed=7490284;
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THBS4 OR TSP4 OR TSP-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001881; EGF Ca.
InterPro; IPR003629; EGF like.
InterPro; IPR00367; tgp 3.
InterPro; IPR003129; TSPN.
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LAWININ AND TYPE V COLLAGEN.
SUBUNIT: HOMOTRIMER, CROSS-LINKED BY DISULFIDE BONDS
SIMILARITY)
BELONGS TO THE THROMBOSPONDIN FAMILY.
SIMILARITY: Contains 4 EGF-like domains.
SIMILARITY: Contains 7 TSP type-3 domains.
SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
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P.,
                   THROMBOSPONDIN .
N-TERMINAL.
EGF-LIKE 1.
EGF-LIKE 2, CALG
EGF-LIKE 3, CALG
EGF-LIKE 4.
TSP TYPE-3 1.
TSP TYPE-3 2.
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Query Match:
DB:
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DO
  MEDLING-87089740; PubMed=2432395;
MEDLING-87089740; PubMed=2432395;
Eichinger D.J., Arnot D.E., Tam J.P., Nu
                                                                                                                                                              01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Circumsporozoite protein precursor (CS
Plasmodium berghei.
Eukaryota; Alveolata; Apicomplexa; Hae
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P06915;
                                                                                                                                        NCBI_TaxID=5821;
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BY SIMILARITY.
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                                                                                                                                                                          Haemosporida;
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                                       Nussenzweig
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CRC64;
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P23093;
01-NOV-1991
                                                                                                                                                                                                                                                            PLABA
SEQUENCE FROM N.A.

MEDLINE=90221834; PubMed=2183186;
LOCKYET M.J., Davies C.S., Suhrbier A., Sinden
"Nucleotide sequence of the Plasmodium berghei
protein gene from the ANKA clone 2.34L.";
Nucleic Acids Res. 18:376-376(1990)
-j-FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS 7
SURFACE ANTIGEN ON THE SPOROZOITE (THE INFE
                                                                                                                                          01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence
28-FEB-2003 (Rel. 41, Last annotati
Circumsporozoite protein precursor
Plasmodium berghei (strain Anka).
Eukaryota; Alyeolata; Apicomplexa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M14135; AAA29577.1; -.
PIR; A44948; OZZOMB.
InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR000884; TSP1.
Pfam; PF00090; tsp_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         identification of the immunodominant epitopes."; Mol. Cell. Biol. 6:3965-3972(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF TH MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Contains 1 TSP type-1 domain.
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- PP01303; CRCMSPRZOITE.
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                                                                                                                                                                                                                                                                                                                                                         Sporozoite;
                                                                                                                                                                                                                                                                                                                             CCGGAACCGGAAGGTACCGGATCATCAGAAAAAGAT 333
                                                                                                                                                                                                                                                                                                   ProGlnProGlyGlyAsnAsnAsnAsnLysAsnAsn
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Last annotation update
ein precursor (CS).
                                                                                                                                            Apicomplexa; Haemosporida; Plasmodium
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CIRCUMSPOROZOITE PROTEIN.

13 X 8 AA TANDEM REPEATS.

16 X 2 AA TANDEM REPEATS O

TSP TYPE-1.
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Matches:
Conservative:
Mismatches:
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    INFECTIVE
                THE IMMUNODOMINANT
                                                      R.E.;
circumsporozoite
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    STAGE OF THE
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RESULT
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01-MAR-1989
01-MAR-1989
01-APR-1993
MEDLINE=88274327; PubMed=2839594;
MCGeoch D.J., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C.,
MCGab D., Perry L.J., Scott J.E., Taylor P.;
"The complete DNA sequence of the long unique region in the genome
herpes simplex virus type 1.";
J. Gen. Virol. 69:1531-1574(1988).
-i- FUNCTION: TECUMENT PROTEIN.
-i- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36,
EHV-1 24, EBV BPLF1, HVS-1 64, VZV 22, AND HCMV UL48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Herpes simplex virus (type 1 / strain 17)
Viruses; dsDNA viruses, no RNA stage; Her
Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro, 150 1; 1. Pfam; PF00090; tsp 1; 1. P
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                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S07873; OZZQBK.
InterPro; IPR003067;
InterPro; IPR000884;
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ANCHORING THE PROTEIN TO THE CELL MEMBRANE. T
WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
SIMILARITY: Contains 1 TSP type-1 domain.
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347
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(Rel. 10, Last sequence update)
(Rel. 25, Last annotation update)
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23 POTENTIAL.
47 CIRCUMSPOROZOITE PROTEIN.
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17 X 2 AA REPEATS OF P-Q.
                                                                                                                                                                                                                                                                                                                                                                                     protein UL36).
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                       RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Ra Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Ra Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Ra Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Ra Kuchl P., Lewis S., Matsuc Y., Nikaido I., Pesole G., Quackenbush J., Ra Kuchl P., Lewis S., Matsuc Y., Nikaido I., Pesole G., Quackenbush J., Ra Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Ra Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Ra Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Ra Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Ra Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Ra Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Ra Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Ra Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Ra Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Ra Wynshaw-Borts A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Ra Wynshaw-Borts A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Ra Wang K.H., Weitz C., Whittaker C., Wilming L., Ra Wynshaw-Borts A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Ra Wang K.H., Weitz C., Whittaker C., Wilming L., Ra Wynshaw-Borts A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Ra Wang K.H., Weitz C., Whittaker C., Wilming L., Ra Wang K.H., Weitz C., Whittaker C., Wilming L., Ra Wang K.H., Weitz C., Whittaker C., Wilming L., Ra Wang K.H., Weitz C., Whittaker C., Wilming L., Ra Wang K.H., Weitz C., Whittaker C., Wilming L., Ra Wang K.H., Weitz C., Whittaker C., Wilming L., Ra Wang K.H., Weitz C., Whittaker C., 
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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MEDLINE=21085660; PubMed=11217851;
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28-FEB-2003 (Rel. 41,
28-FEB-2003 (Rel. 41,
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-!- SUBCELLULAR LOCATION: Nuclea
-!- SIMILARITY: Contains 1 CARD
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-!- FUNCTION: May be involved in RNA splicing (By similarity).
-!- SUBUNIT: Interacts with SRp30c, NPM1, CASP2, CASP8 and CED-3
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SMART; SM00114; CARD; 1.
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Haque N.S., Buchberg A.M., Khalili K.;
"Isolation and characterization of MRF-1, a brain-derived DNA-L
protein with a capacity to regulate expression of myelin basic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Nuclear (By similarity).
TISSUE SPECIFICITY: EXPRESSED IN ALL THE TISSUES EX
KIDNEY, SPLEEN, HEART, LUNG, AND BRAIN).
PTM: EXTENSIVELY PHOSPHORYLATED ON SERINE RESIDUES
DOMAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE SR FAMILY OF SPLICING FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tiol. Chem. 269:31149-31156(1994).
FUNCTION: CAN BIND TO THE MYELIN BASIC PROTEIN REGULATORY REGION AND INCREASE TRANSCRIPTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGI:104846;
                                                                                                                                                         189
 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U14648; AAA64595.1; -.
                                                                                                                                                                                      98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CELLS DERIVED FROM THE CNS.
                                                                                                           ACGTGCGGGACTGGCTGCGGCAGCAGGTCAGGGAGATCACGTTCCTGAAAAAACACGGTGA
                                                                                                                                                                                                                   SerProArgArgProAlaAlaAlaIleSerLysProGlu------ 188
CGCAGCCGAAACCGCAGCCGAAACCGGAACCGGAAGGTACCGGATCATCAGAAAAAAGATG 334
                                                            TGGAGTGTGACGCGT---GCGGGCCGCAGCCGCAGCCGAAACCGCAGCCGCAGCCGCAGC
                                                                                                                                                                                    GTTCAGACCTGGGCCCGCAGATGCTTCGGGAACTGCAGGAAACCCAACGCGGCGCTGCAGG 157
                                                                                                                                                                                                                                                  TCGCCCTTGCGGCAGTCTGCAGCGCTGCCAAAAAAAGGATCCAGCCTGGGTGGAGACTGTT 97
                           ThrSerLysSerArgSerAlaArgArgSerLysSerLysSerSerSerValSerArgSer
                                                                                                                                                                                                                                                                                                                                                                                                                                           283 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           167
173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNA-binding;
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122.00
57.01%
39.25%
18.15%
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172 G
259 A
31581 MW;
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                                                                                           -----LysserArgSer---ArgThrArgSer---ArgSerArgSer 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLY-RICH (HINGE REGION) ARG/SER-RICH (RS DOMAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                       NG/SER-RICH (RS DOMAIN).
OB4EB2C9CC9172AE CRC64;
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Matches:
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Mismatches:
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basic protein
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                                                    Signal;
PROPEP
DOMAIN
                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                     Clayton C.E., Mowatt M.R.;
"The procyclic acidic repetitive proteins of Tryp
Purification and post-translational modification.
J. Biol. Chem. 264:15088-15093(1989).
                                                                                                                                                                                                                                                                                                                                                                                                            Vijayasarathy S., Ernest I., Itzhaki J., Sherman D., Mov
Michels P.A.M., Clayton C.E.;
Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clayton C.E., Fueri J.P., Itzhaki J.E., Bellofatto Wisdom G.S., Vijayasarathy S., Mowatt M.R.; "Transcription of the procyclic acidic repetitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=87115776; PubMed=3808022;
Roditi I., Carrington M., Turner M.;
"Expression of a polypeptide containing a dipeptide r confined to the insect stage of Trypanosoma brucei.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trypanosoma brucei brucei.
Eukaryota; Euglenozoa; Kin
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                                                                                       EMBL; X04814; CAA28503.1; -.
EMBL; M33129; AAA30225.1; -.
EMBL; X52584; CAA36815.1; -.
                                                                                                                                           or send
                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trypanosoma
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                                                                                                                                                                                                                                                                                                                                                           MEDLINE=89359323; PubMed=2475493;
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                                       CHAIN
                                                                                                                                                                                                                                                 Biol. Chem. 264:15088-15093(1989).
FUNCTION: MAJOR SURFACE ANTIGEN OF PROCYCLIC FORMS.
SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
DEVELOPMENTAL STAGE: EXPRESSED ONLY AT A CERTAIN STAGE DURING
DIFFERENTIATION IN THE INSECT VECTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell. Biol.
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                                                                                                                                           s requires a license agreement (S an email to license@isb-sib.ch).
                                                     Antigen; Repeat;
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(Rel. 10, Last sequence update)
(Rel. 40, Last annotation update)
xrm specific polypeptide A-beta pr
 108
59
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                                                               Glycoprotein;
                           BETA
 24 X 2
                                       PROCYCLIC
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 TANDEM REPEATS OF [DE] - P
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                                                                                                                                                                                   as its content
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                                       SPECIFIC POLYPEPTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein genes
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Percent Similarity:
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                                  Pylori.",
Nature 388:539-547(1997).

Nature 388:539-547(1997).

-I. FUNCTION: INTERACTS WITH OUTER MEMBRANE RECEPTOR PROTEINS THAT CARRY OUT HIGH-AFFINITY BINDING AND ENERGY DEPENDENT UPTAKE INTO THE PERIPLASMIC SPACE OF SPECIFIC SUBSTRATES. IT COULD ACT TO TRANSDUCE ENERGY FROM THE CYTOPLASMIC MEMBRANE TO SPECIFIC ENERGY-REQUIRING PROCESSES IN THE CYTOPLASMIC MEMBRANE, RESULTING IN THE RELEASE INTO THE PERIPLASM OF LIGANDS BOUND BY THESE OUTER MEMBRANE PROTEINS (BY SIMILARITY).

-I. SUBCELLULAR LOCATION: ANCHORED TO THE CYTOPLASMIC MEMBRANE VIA ITS N-TERMINAL SIGNAL-LIKE SEQUENCE, SPANS THE PERIPLASM (BY SIMILARITY).
                                                                                                                                                                                                                         STRAIN=26695 / ATCC 700392;

STRAIN=2695 / ATCC 700392;

STRAIN=2695 / ATCC 700392;

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,

Pleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.

Relson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,

Nelson K., Quackenbush J., Dodson R., Khalak H.G., Glodek A.,

Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,

McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,

Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.

Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin

Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
LIPID
SEQUENCE
 This SWI
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                              Helicobacteraceae; Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                         Helicobacter pylori (Campylobacter pylori)
Bacteria; Proteobacteria; Epsilonproteobac
                                                                                                                                                                                                                                                                                                                                                                                                                                   TONB OR HP1341.
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15-DEC-1998 (Rel. 37,
16-OCT-2001 (Rel. 40,
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                                                                                                                                                                                                     complete genome sequence of the
             SWISS-PROT entry is
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copyright. It is produced through a c
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Indels:
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Matches:
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                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1990 (Rel. 14, Createo)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transport; Protein transport; Inner membrane; Periplasmic Transport; Protein transport; Inner membrane; Periplasmic Transmembrane; Signal-anchor; Repeat; Complete proteome. DOMAIN 1 1 4 CYTOPLASMIC (POTENTIAL). TRANSMEM 15 35 SIGNAL-ANCHOR (POTENTIAL). DOMAIN 36 285 PERIPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                 -I- FUNCTION: MAJOR SURFACE ANTIGEN OF PROCYCLIC FORMS.
-I- SUBCELLULAR LOCATION: Attached to the membrane by a GPI
-I- DEVELOPMENTAL STAGE: EXPRESSED ONLY AT A CERTAIN STAGE
DIFFERENTIATION IN THE INSECT VECTOR.
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MEDLINE=90067841; PubMed=2573878;
Koenig E., Delius H., Carrington M
"Duplication and transcription of
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01-AUG-1988
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"Developmental regulation of a novel repetitive protein of
"Typanosoma brucei.";

Trypanosoma brucei.";

Mol. Cell. Biol. 7:2838-2844(1987).

-i- FUNCTION: MAJOR SURFACE ANTIGEN OF PROCYCLIC FORMS.

-i- FUNCTION: MAJOR SURFACE ANTIGEN OF PROCYCLIC FORMS.

-i- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.

-i- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.

DIFFERENTIATION IN THE INSECT VECTOR.
                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstati the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
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DOMAIN. ...
SEQUENCE
                                                                                   01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
Procyclic form specific polypeptide B-alpha precursor (Procyclin)
(PARP B-alpha) (PSSA-1).
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                     Vijayasarathy S., Ernest I., Michels P.A.M., Clayton C.E.. Submitted (JUN-1992) to the I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MRDLINE=90258895, PubMed=2342468;
Clayton C.E., Fueri J.P., Itahaki J.E., Bellofatto
Wisdom G.S., Vijayasarathy S., Mowatt M.R.;
"Transcription of the procyclic acidic repetitive p
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EMBL; L02933; AAA30228.1; -.
PIR; A44418; A44418.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal; Antigen; Repeat; Glycoprotein; GPI-anchor.
SIGNAL 1 27 BY SIMILARITY.
CHAIN 28 123 PROCYCLIC FORM SPECIF
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GPI-ANCHOR (BY SIMILARITY).
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Post-processing: Minimum Match 0%
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-Q=/cgn2_1/USPTO_spool/US0996872/runat_26082003_150542_8726/app_query.fasta_1.519
-Q=-(cgn2_1/USPTO_spool/US0996872/runat_26082003_150542_8726/app_query.fasta_1.519
-DB=SPTREMBL_23_-QFMT=fastan_SUFFIX=xspt_-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits_START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-UTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09696872_@CGN_1_1_172_@runat_26082003_150542_8726 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-DEV_TIMEDUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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1: sp_archea:

2: sp_bacteri

3: sp_fungi:*

4: sp_human:*
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sp_vertebrate:*
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                                                                                                                                         InterPro; IPRO02048; EF-hand.
InterPro; IPRO01881; EGF Ca.
InterPro; IPRO01809; EGF like.
InterPro; IPR005209; EGF like.
InterPro; IPR005367; tsp 3; 10-
SMART; SM00179; EGF CA; 2.
PROSITE; PS001019; EF HAND; 1.
PROSITE; PS01186; EGF CA; 2.
EGF like domain; Matrix protein
SEQUENCE 755 AA; 92162 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

Dudhia J., Williams D., Smith R.K.;

Dudhia J., Williams D., Smith R.K.;

"Molecular characterization and tissue distribution of (
cartilage oligomeric protein (thrombospondin 5).";

Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases

EMBL; AF325902; AAG59881.1; -.
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Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
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01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2003 (TrEMBLrel. 23,
Cartilage oligomeric matrix
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Last annotation update)
protein.
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                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

A Lamerdin J.E., McCready P.M., Adamson A.W., Burkhart-Schultz K.,

A Gordon L., Kyle A., Ramirez M., Stilwagen S., Garnes J., Danganar

A Christensen M., Bruce R., Quan G., Montgomery M., Ow D., Kobayasi

A Christensen M., Bruce R., Quan G., Montgomery M., Ow D., Kobayasi

A Christensen M., Bruce R., Quan G., Montgomery M., Ow D., Kobayasi

A Christensen M., Bruce R., Quan G., Montgomery M., Ow D., Kobayasi

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A Christensen M., Bruce R., Quan G., Montgomery M., Ow D., Kobayasi

A Christensen M., Bruce R., Quan G., Montgomery M., Ow D., Kobayasi

BemBL, Accoston G., Carrano A.V.;

I Sequence A.V.;

A Christensen M., Bruch G., Montgomery M., Ow D., Kobayasi

A Christensen M., Bruch G., Montgomery M., Ow D., Kobayasi

A Christensen M., Bruch G., Carle M., Stillagen M., Carle M., Stillagen M., Stillagen M., Carle M., Stillagen M
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01-JAN-1998
01-MAR-2003
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
MCBI_TaxID=9606;
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Y "Molecular Cloning, Sequencing, Tissue and Developmental Expression of YT Mouse Cartilage Oligomeric Matrix Protein (COMP).";

L. J. Orthop. Res. 0.0-0(1999).

R EMBL; AF033530; AAD01972.1; -.

DR HSSP, P35444; YUDF.

DR MGD; MGI-88469; Comp.

DR InterPro; IPR002048; EF-hand.

DR InterPro; IPR001881; EGF_Ca.

DR InterPro; IPR001881; EGF_Like.

DR InterPro; IPR00357; tsp_3.

DR SMART; SM00179; EGF_CA; 2.

DR PROSITE; PS01187; EGF_CA; 2.

DR EGF-Like domain; Matrix protein; Signal.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pang C. Leslie M.P., Nord R., Tian H., Di Cesare P.E.;

"Mouse Cartilage Oligomeric Matrix Protein Genomic Sequence
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

IR EMBL, AP257516; AAL36518.1; -

IN InterPro; IPR002048; EF-hand.

InterPro; IPR00181; EGF Ca.

InterPro; IPR001367; tsp_3.

InterPro; IPR003367; tsp_3.

InterPro; IPR003167; tsp_3.

InterPro; IPR003167; tsp_3.

IN Pfam; PF02412; tsp_3; 9.

IN Pfam; PF02412; tsp_3; 9.

IN PROSITE; PS01186; EGF CA; 2.

IN PROSITE; PS01186; EGF CA; 2.

IN PROSITE; PS01186; EGF CA; 2.

IN PROSITE; PS01187; EGF CA; 2.

IN EGF-1ike domain; Matrix protein.

Q SEQUENCE 755 AA; 82286 MW; 91758FCF789167EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cartilage oligomeric matrix
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata
Mammalia; Eutheria; Rodentia
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                  CTGCAGGAAACCAACGCGGCGCTGCAGGACGTGCGGGACTGGCTGCGGCAGCAGGTCAGG
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                                                                      CCGAAACCGCAGCCGCAGCCGCAGCCGAAACCGCAGCCG
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                                                                                                                                                                                                                                                                                                                                                     AAAGGATCCAGCCTGGGTGGAGACTGTTGTTCAGACCTGGGCCCGCAGATGCTTCGGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                            MetGlyProThrAlaCysValLeuValLeuAlaLeuAlaIleLeuArgAlaThrGlyGln
                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGGGAAGGTACATGATTTTAGGCTTGCTCGCCCTTGCGGCAGTCTGCAGCGCTGCCAAA
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66.32%
56.84%
35.42%
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein.
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Sciurognathi; Muridae;
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002048; EF-hand.
InterPro; IPR0018B1; EGF Ca.
InterPro; IPR006209; EGF like.
InterPro; IPR006210; IEGF.
SMART; SM00181; EGF; 4.
SMART; SM00179; EGF CA; 3.
PROSITE; PS00118; EF HAND; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01187; EGF CA; 2.
                                                                                                                      O94885 PRELIMING.,
O94885,
O1-MAY-1999 (TrEMBLrel. 10, Created)
O1-MAY-1999 (TREMBLrel. 10, Last sequence update)
O1-MAY-2003 (TrEMBLrel. 23, Last annotation update)
O1-MAR-2003 (TrEMBLREL 23, Last annotation update)
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Q8N4T2;
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to cartilage oligomeric matrix protein (pseudepiphyseal dysplasia 1, multiple).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
 MEDLINE=99087487; PubMed=9872452;
Nagase T., Ishikawa K., Suyama M.,
Kotani H., Nomura N., Ohara O.;
"}rediction of the coding sequence
                                                SEQUENCE FROM N.A.
TISSUE=Brain;
                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases EMBL; BC033676; AAH33676.1; -
                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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195.50
79.63%
75.93%
29.09%
                                                                                            Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79696 MW;
 sequences
                                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                       Kikuno R.,
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                       Miyajima
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41
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human genes.
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                        Tanaka
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PROMETER AND PROME
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Best Local Similarity:
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Q9QYS3;
01-MAY-2000 (TrEMBLrel. 13, C
01-MAY-2000 (TrEMBLrel. 13, L
01-MAR-2003 (TrEMBLrel. 23, L
Thrombospondin 4 (Fragment).
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=99431670; PubMed=10501972;
MORTON C.
                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia, Eutheria, Rodentia,
                           "The thrombospondin-4 gene.", Mamm. Genome 10:1010-1016(1999). EMBL; AF152393; AAD32714.1; -EMBL; AF152392; AAD32714.1; JOINI EMBL; AAD32714.1; AA
                                                                                                                                                                                                  Newton G., Weremowicz S., Copeland N.G., Lawler J.;
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Pfam; PF00018; SH3; 1.
SMART; SM00454; SAM; 2.
SMART; SM00326; SH3; 1.
SMART; PS50105; SAM DOMAIN;
HYDOT PS511 PS51517
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                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The complete sequences of 100 new cDNA clones from brain which for large proteins in vitro.";
DNA Res. 5:277-286(1998).
                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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   MGI:1101779; Thbs4
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Sciurognathi; Muridae;
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Pfam; PF02412; tsp3; 9.

Pfam; PF02412; tsp3; 9.

SMART; SM00179; EGF CA; 2.

SMART; SM00210; TSPN; 1.

PROSITE; PS00118; EF HAND; 1.

PROSITE; PS01186; EGF 2; 1.

PROSITE; PS01187; EGF CA; 2.
                                                                                                                                                                                                                                                                                                               01-MAY-1999
01-MAY-1999
01-MAR-2003
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Q9Z1T2;
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                                                                Newton G., Weremowicz S., Morton Copeland N.G., Lawler J.;
"The thrombospondin-4 gene.";
Mamm. Genome 10:1010-1016(1999).
EMBL; AF102887; AAC73003.1; -.
HSSP; P35444; IVDF.
                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Eukheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=99431670; PubMed=10501972;
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InterPro; IPR001881; EGF_Ca.
InterPro; IPR006209; EGF_like.
InterPro; IPR003129; TSPN.
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                                                   MGD; MGI:1101779; Thbs4.
                                     InterPro;
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IPR002048; EF-hand.
IPR001881; EGF_Ca.
IPR006209; EGF_like
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(TrEMBLrel. 10, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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Sciurognathi; Muridae;
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SEQUENCE
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01-NOV-1996
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                                                    SEQUENCE FROM N.A.

MEDLINE-87218962; PubMed=3556207;
Webber J.L., Egan J.E., Lyon J.A., Wirt
Maloy W.L., Hockmeyer W.T.;
"Plasmodium berghei: Cloning of the ci
Exp. Parasitol. 63:295-300(1987).

EMBL; M25445; AAA22531.1; -

InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR002965; Prich_extensn.
InterPro; IPR002965; TSP1.

Pfam; PF00303; TSP1.

Pfam; PF00303; TSP1.

PRINTS; PR01313; PRCMSPRZOITE.
PRINTS; PR01303; TSP1; 1.

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InterPro; IPR003367; tsp_3.
Pfam; PF000008; EGF; 1.
Pfam; PF002210; TSPN; 1.
Pfam; PF002210; TSPN; 1.
Pfam; PF002412; tsp_3; 9.
SMART; SM00210; TSPN; 1.
PROSITE; PS001018; EF HAND; 1.
PROSITE; PS001186; EGF 2; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01187; EGF_CA; 2.
EGF-like domain.
SEQUENCE 963 AA; 106366 MW;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Circumsporozoite (CS) protein (Fragment).
Plasmodium berghei.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                 PROSITE; PS50092; TSP1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Sequence of the circumsporozoite gene of Plasmodium ber clone and NK65 strain.";
Mol. Biochem. Parasitol. 39:151-154(1990).
REMBL, W28887, AAA29541.; -.
InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR002965; P_rich_extensn.
InterPro; IPR002965; P_rich_extensn.
InterPro; IPR0029684; TSP1.
REMINTS; PR01303; CRCMSPRZOITE.
PRINTS; PR01303; CRCMSPRZOITE.
PRINTS; PR013017; PRICHEXTENSN.
  Q69088;
01-NOV-1996
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Q25649; PREMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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PROSITE; PS50092; TSP1; 1.
SEQUENCE 332 AA; 36196 MW;
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Eukaryota; Alveolata;
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  sequence update)
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"The complete DNA sequence of the long unique recherges simplex virus type 1.",
J. Gen. Virol. 69:1531-1574(1988).

EMBL, D10879; BAA01682.1;
- InterPro; IPR005210; Herpes teg_N.
InterPro; IPR005210; Herpes Ul36.
Pfam; PF04843; Herpes Ul36; 1.
Pfam; PF04843; Herpes Ul36; 1.
SEQUENCE 3164 AA; 335817 MW; 2E3335F9525F8C7
                                     Pfam; PF01483; P; 1.
Pfam; PF00082; Peptidase S8; 1.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR0723; SUBTILISIN.
ProDom; PD000717; P domain; 1.
PROSITE; PS00137; SUBTILASE_HIS; 1
Protease.
SEQUENCE
                                                                                                                                                                                                                                                                  STRAIN-Pneumocystis carinif f. sp. carini; Seeger K., Quail M., Harris D., Hall N., Wakefield A., S Cushion M.T., Stringer J.R., Kell S., Barrell B.G.; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases. i- SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN. EMBL, AL592263; CAC42801.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pneumocystis carinii.
Eukaryota; Fungi; Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probable protease 1 like PCCW01B2.03.
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Alphaherpesvirinae; Simp
NCBI_TaxID=10298;
                                                                                                                                                                               InterPro; IPR000209;
InterPro; IPR002884;
InterPro; IPR002965;
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Simplexvirus.
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0B8EF527C4D9603A CRC64;
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STRAIN=cv. CP72-2086; TISSUE=Leaf;
Yang M., Paterson A.H., Mirkov E.T.;
Yang M. paterson a.H., Mirkov E.T.;
"A rapid and direct approach to find promoters for driving gene expression in sugarcane.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                        EMBL; AF331852; AAM/18423.1; -..
Interpro; IPR002965; P rich ex
PRINTS; PR01217; PRICHEXTENSN.
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STRAIN=cv. CP72-2086; TISSUE=Leaf;
Yang M., Paterson A.H., Mirkov E.T.;
"Cloning and characterization of a proline-rich protein gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum.
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MEDLINE=96123388; PubMed=8577324;
Toye P., Gobright E., Nyanjui J., Nene V., Bishop R.;
"Structure and sequence variation of the genes encoding polymorphic, immunodominant molecule (PIM), an antigen o parva recognized by inhibitory monoclonal antibodies.";
Mol. Biochem. Parasitol. 73:165-177(1995).
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